

Access DB# 32383

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

FOR OFFICIAL USE ONLY

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Ed Dean - July</u>	NA Sequence (#) <u>4</u>	STN _____
Searcher Phone #: <u>308-4501</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Biotec Lib.</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>1/4/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>1/17/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>AB5501</u>
Clerical Prep Time: <u>5 min</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>2 min</u>	Other _____	Other (specify) _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 19:06:42 ; Search time 6198.48 Seconds

(without alignments)
695.102 Million cell updates/sec

Title: US-09-180-798-30
Perfect score: 1063
Sequence: 1 tcgaccacagctccgacga.....tgcaaaaaaaaaaaaaa 1063

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202661650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
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105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

8
Query

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	465.8	43.8	469	63	A1992866
2	395.9	37.2	556	63	R89998
3	373.4	35.1	442	42	A1100481
4	358	33.7	360	42	A1100685
5	349.4	32.9	364	42	A1100683
6	336.8	31.7	534	33	AA3943359
7	332	31.2	348	43	A1100682
8	329.2	31.0	401	37	AA712221
9	328.2	30.8	353	33	H37300
10	318.2	29.9	608	81	AW443205
11	317.2	29.8	720	62	AW031110
12	314.6	29.6	339	42	A1100679
13	302.4	28.4	447	23	H36600
14	301.4	28.4	336	23	H37296
15	301	28.3	646	74	AW211939
16	297.6	28.0	657	80	AW350720
17	296.8	27.9	511	74	AW221278
18	293.4	27.6	714	64	AW030188
19	292.6	27.5	336	62	A1100680
20	286.8	27.0	336	20	H34187
21	281.6	26.5	334	23	H37195
22	280	26.3	695	64	AW028168
23	278.6	26.0	305	25	N63416
24	276	26.0	599	63	AW011134
25	274	25.8	559	74	AW2119797
26	268.8	25.3	304	36	T21150
27	265.4	25.0	637	80	AW350549
28	264	24.8	465	45	A1352795
29	261.4	24.6	676	75	AW230075
30	257.6	24.2	430	79	AW2307218
31	257.4	24.2	569	59	A1775448
32	253.4	23.8	258	42	A1100678
33	246	23.1	545	64	AW037836
34	244.2	23.0	337	20	Z34606
35	242.4	22.8	522	46	A1441759
36	237.8	22.4	667	74	AW185847
37	235.2	22.1	541	64	AW046885
38	233.6	22.0	619	64	AW040482
39	232.8	21.9	612	47	A1436335
40	228.4	21.5	423	35	C22371
41	226.6	21.3	515	79	AW279515
42	225.8	21.2	570	50	A1676939
43	222.6	20.9	568	47	A1487272
44	221.4	20.8	616	42	AF074734
45	220.4	20.7	265	23	R84144

ALIGNMENTS

TITLE	Hanson, D.				
JOURNAL	Arabidopsis thaliana Gene Expression MicroArray				
COMMENT	unpublished (1999)				
	On Dec 20, 1995 this sequence version replaced g1:1135328.				
	Contact: David Smoller, Ph.D.				
	Genome Systems, Inc., a wholly owned subsidiary of Incyte				
	Pharmaceuticals, Inc.				
	4633 World Parkway Circle, St. Louis, MO 63144, USA				
	Tel: 877-577-2733				
	Fax: 314-427-3324				
	Email: service@genomesystems.com.				
FEATURES					
source	location/Qualifiers				
	1..469				
	/organism="Arabidopsis thaliana"				
	/db_xref="taxon:3702"				
	/clone="701493826"				
	/clone_lib="A. thaliana, Ohio State clone set"				
	/note="cDNA library was made from selected clones from the				
	Arabidopsis thaliana Ohio State clone set."				
BASE COUNT	120 a	124 c	89 g	136 t	
ORIGIN					
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Best Local Similarity	99.6%;	Fred. No. 5.5e-108;			
Matches 467;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	17	acgaaccccaatttgccttcctcatctgtttcagaanaattactcaattccattagat	76		
Db	1	ACGAACCCCAATTTCCTTCCTCATCTGTTCAGAAATATACCAAAATTCCTATTNAGAT	60		
QY	77	tactctcttcgaacctcgatagatcacaatgagcgtcgcgaacctatcggtyggagctt	136		
Db	61	TACTCTTCCTTCGACCTCCGATGACTCAAGAGCGGTTCGAAATATACGCTGGAGCTCT	120		
QY	137	tcgcagcttcgttaatccccaacctagatttggatgaacctgtrtgcgaaggaacctcgaag	196		
Db	121	TCCGAGCTTCGTTAATCCTTAACCTTAGCTTTGATTCACCTGTCGAAACCAACTCCGAAG	180		
QY	197	gagatgctcttaacgtctcttcgcgcggaatttaacagatccggagacatgcttccagaagt	256		
Db	181	GAGATGCTTCCTTACGCTTCGCCGGAATTAAAGATCCGAGACATGTTCTCCAGAGCT	240		
QY	257	ggagatcaacctctgttgaatcctctgacctggttccatgctacactgtaaccaagaacaac	316		
Db	241	GGAATCCAACTCTTGTAATCCTTGACTGATGATCCAGTCAATGATCACTGTAAACCAAGACAAAC	300		

RESULT	1
LOCUS	AI1992868
DEFINITION	AI1992868 469 bp mRNA EST 08-SEP-1999
ACCESSION	701493826 A. thaliana, Ohio State clone set Arabidopsis thaliana
VERSION	AI1992868
KEYWORDS	CDNA clone 701493826, mRNA sequence.
SOURCE	AI1992868.1 GI:5839773
ORGANISM	EST. thale cress. Arabidopsis thaliana Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II: Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 469) Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouaoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kasuriy, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobritiga, A., Murry, L., Turner, C., Kirkorian, S., Elder, L. and
REFERENCE	
AUTHORS	

Accession	Version	Keywords	Source	Organism
Db	361	GGAAGCTTGAACTTTACAGTATCTAGAGCTTACACATACACATCCAGGAATATATAC	420	
Oy	437	cttcgcgaacttggaaatctgaaagaatctcatcagcttggatctgtcaaca	485	
Db	421	CTTCCGAACCTTGGAATCTGAAATCGAAGATCTCATCGCTTGATCTGTACAA	469	
Result	2			
Locus	R89998	556 bp	mRNA	EST
Definition	16353	Lambda-PRL2	Arabidopsis thaliana	CDNA clone 187H577, mRNA
Accession	R89998			
Version	R89998.1	GI:957538		
Keywords	EST.			
Source	thale cress.			
Organism	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eudicots II; Brassicales; Brassicaceae;			

REFERENCE 1 (bases 1 to 556)
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
 McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasnow,M.,
 Retzel,E. and Somerville,C.
 TITLE Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)
 MEDLINE 95148729
 COMMENT On Apr 14, 1993 this sequence version replaced gi:693023.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcn@dm.cl.msu.edu
 Seq primer: T7 dye primer.
 Location/Qualifiers
 1..556
 /organism="Arabidopsis thaliana"
 /strain="var columbiana"
 /db_xref="taxon:3702"
 /clone="187H5T7"
 /clone.lib="lambda-PRU2"
 /note="Vector: lambda Zip-lox; Site_1: Sal; Site_2: Not;
 lambda PRU2 is a cDNA library derived from equal
 quantiles of 4 pools of mRNA. The mRNA sources were 1) 7
 day germinated etiolated seedlings; 2) tissue culture
 grown roots; 3) staged plants half with 24 hour light
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
 same plants as 3 but aerial tissue (stems, flowers and
 siliques. The vector is BRU's lambda Zip-lox. The cDNA
 inserts were directionally cloned with Sal-Not arms using
 oligo dt primed cDNA. " 118 c 123 g 146 t 18 others

BASE COUNT 151 a 118 c 123 g 146 t 18 others
 ORIGIN

Query Match 37.2%; Score 395.4; DB 23; Length 556;
 Best Local Similarity 94.4%; Pred. No. 4e-90;
 Matches 441; Conservative 0; Mismatches 20; Indels 6; Gaps 3;

OY 349 ctctctgacatcttgctgagcttgaggaagcttgaacattatcagatcagagtc 408
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 Db 1 CTCCTGTGACATCTTGGCGCTGAGCTTGGAGACTTGAACATTACATATCTAGAGCTC 60
 OY 409 tacaaaaacaacatccaagaactatactccgaacttggaaatctgaagaatctc 468
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 Db 61 TACAAAAACAACATCCAGAGACTATACCTTCGGAACCTTGAATCTGAAGAATCTCATC 120
 OY 469 agcttgatctgtacaaacaacatctacagagatgttccactcttgggaaatgt 528
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 Db 121 AGCTTGATCTGTACAAACAACATCTTACAGGATGATTCCTCCCTTGGGAAATATG 180
 OY 529 aagtcctgtctctttaaaggcttaatgacaacggatgacggagccatccctagagca 588
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 Db 181 AAGTCTCTGGCTTTTAAAGCTTAATGACACGATTCAGCGGCGCAATCCCTAGAGCA 240
 OY 589 ctcaactgcatcccaagccttaaaagtgtgatgtctcaagcaatgattgtgtgaaaca 648
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 Db 241 CTCACCTCAATCCCAACCTTAAAGTGTGATGTCTCAAGCAATATTTGTGTGNAACA 300
 OY 649 atcccaacaacgagactttgtcatcattccttcaagaacttgaagacaacccgag 708
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 Db 301 ATCCCAACAACGAGACCTTTTGTCTCAATCTTTACAGACTTTGAGNACAACCCGAGG 360
 OY 709 ttgg-aaggagcggaaatctactcggtcttgaagctacgacactaactgcacactgaaanaa 767
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 Db 361 TTGGNAGGAGACCGGAATTAATCTCGGTCTTGAACGCTNCGGCAATTAATGACCC--TGAAAA 417
 OY 768 ttggcaaacactggaatgaagaattgggggggagacttgaagaac 814

Db 418 ATTGAAACCTGAAA--TGAGATTGGGGGTGNCCTTTAAGGCAC 462
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 RESULT 3
 AII00481
 LOCUS AII00481 442 bp mRNA EST 21-NOV-1998
 DEFINITION 34856 Lambda-PRU2 Arabidopsis thaliana cDNA clone 90J7XP 3', mRNA
 sequence.
 ACCESSION AII00481
 VERSION AII00481.1 GI:3450442
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.
 1 (bases 1 to 442)
 /organism="Arabidopsis thaliana"
 /strain="var columbiana"
 /db_xref="taxon:3702"
 /clone="90J7XP"
 /clone.lib="lambda-PRU2"
 /note="Vector: lambda Zip-lox; Site_1: Sal; Site_2: Not;
 lambda PRU2 is a cDNA library derived from equal
 quantiles of 4 pools of mRNA. The mRNA sources were 1) 7
 day germinated etiolated seedlings; 2) tissue culture
 grown roots; 3) staged plants half with 24 hour light
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
 same plants as 3 but aerial tissue (stems, flowers and
 siliques. The vector is BRU's lambda Zip-lox. The cDNA
 inserts were directionally cloned with Sal-Not arms using
 oligo dt primed cDNA. " 135 a 82 c 90 g 132 t 3 others

BASE COUNT 135 a 82 c 90 g 132 t 3 others
 ORIGIN

Query Match 35.1%; Score 373; DB 42; Length 442;
 Best Local Similarity 93.0%; Pred. No. 1.9e-84;
 Matches 411; Conservative 0; Mismatches 28; Indels 3; Gaps 2;

OY 608 ttaagttgtatgactctcaagcaatgatgtgtggaacaaat-cccaacaacgagact 666
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 Db 1 TAAAGTTNTTGGATTCGTCGCAATGTTGTGGAACAATCCCAACAACGAGACCT 60
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 Db 61 TTGCTCCACATCTCTTTACAGACTTTGAGAACACCCGAGGTGGAGGACCCGGAAT 120
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Db	181	TGAAGAATTGGGGGTCACCTTTAAAGAACACTTCACCACTTATATAAATATCACCTTA	240
OY	845	ctatgtaatgaatataatatagtcagtcacaaaaaaaatgaagaatcgaatcagaatat	904
Db	241	CTATGTAAATAGATATATATATGTAGTCCAAAAAATGAAGAAATCGAATCAGTATAT	300
OY	905	catctgttccaatlgagaacttgggggtctgatatgtaaaaattctaatttgcgaactt	964
Db	301	CATCTGCTCAAAATGAGAACTTTGAGAGTCGTGTATGTAAATTTCTAAATGCGCACTT	360
OY	965	cgcgtactgaatglttcgggttgcggatctcgaagaataacatltglatglatgatat	1024
Db	361	CGCTACTGTAATGTTGCGTTGTGGGATWCTGAGAAGTAACATTGTATGTATGTAT	420
OY	1025	caagtgcttcgctgtctgtcgc	1046
Db	421	CAAGTGTCTGCGCTGTCTTCTGC	442

RESULT	4
A1100685	
LOCUS	A1100685
DEFINITION	A1100685 360 bp mRNA EST 21-AUG-1998
ACCESSION	33806 Lambda-PRL2 Arabidopsis thaliana cDNA clone 90J7XP 3', mRNA sequence.
VERSION	A1100685
KEYWORDS	A1100685.1 GI:3449395
SOURCE	EST.
ORGANISM	thale cress. Arabidopsis thaliana

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
(pages 1 to 360)	Newman, T., deBrujin, F. J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Ralkehl, N., Somerville, S., Thomasow, M., Retzel, E. and Somerville, C.	Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones	Plant Physiol.	106, 1241-1255 (1994)	
				95148729	
				On May 5, 1995 this sequence version replaced g1:797715.	

FEATURES

[illegible]

RESULT	5				
LOCUS	At100683				
DEFINITION	At100683	364 bp	mRNA	EST	21-AUG-1998
ACCESSION	33804	Lambda-PRL2	Arabidopsis thaliana	cdna clone	187H5Xp 3', mRNA
VERSION	At100683				
KEYWORDS	At100683.1	GI:3449393			
SOURCE	EST.				
ORGANISM	thale cress.				
REFERENCE	Arabidopsis thaliana				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Euphylliphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core				
	eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;				
	Arabidopsis				
	1 (bases 1 to 364)				
	Newman,T., debruin,F.J., Green,P., Keegstra,K., Kende,H.,				
	McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,				
	Retzel,E. and Somerville,C.				
TITLE	Genes galore: a summary of methods for accessing results from				
JOURNAL	large-scale partial sequencing of anonymous Arabidopsis cdna clone				
MEDLINE	Plant Physiol. 106, 1241-1255 (1994)				
COMMENT	95148729				
	On May 5, 1995 this sequence version replaced gi:797711.				
	Contact: Thomas Newman				

FEATURES	Location/Qualifiers
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	Location: "Arabidopsis thaliana"

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/clone_id="Lambda-PR2"
/note="Vector: lambda Zip-lox; Site_1: Sal; Site_2: Not;
lambda PR2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRU's lambda Zip-lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA. " 2 others

BASE COUNT 113 a 80 c 70 g 99 t

ORIGIN

Query Match 32.9%; Score 349.4; DB 42; Length 364;
Best Local Similarity 98.9%; Pred. No. 1.8e-78;
Matches 361; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 508 cccactcttgggaaatgaagctctgtcttcttaagcgttaatgaacacgattg 567
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DB 1 CCCATTCTTGGGAAATGAACTGCTTTTACGGCTTATGACAAACCGATTG 59
OY 568 accgggccaatcccttaagcactgcacatcccaagccttaagtgtgtatctca 627
|||||
DB 60 AGGGGGCCAAATCCATGACCTCAGCTCAATCCCAAGCTTAAAGTTGATGCTCTCA 119
OY 628 agcaatgatgtgtggaacaatcccaacaaacgacattgtctcattcttacaag 687
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DB 120 AGCATATGTTGTGTGGACAATCCCAAAAGGACCTTTGCTGCATCTCTTACAG 179
OY 688 aacttgaagaacacccggaggttgagggacgggaattactggtcttgcagactacac 747
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DB 180 AACTTTGAGAAACCCGAGGTTGAGGAGCCGGAATTAATCTCGCTCTTGAACCTAGAC 239
OY 748 actactgcactgaaataatggcaaacctgaaatgaagaattggggggtgacattg 807
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DB 240 ACTAATGCACTGCACTGAAATATGCAAAACCTGAAATGAAATTTGGGGGTGACCTTG 299
OY 808 taagaacactaccacttatacaataatacatctactatgtaataatataatgt 867
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DB 300 TAAAGACACTTCAACCACTTATCAATATCACTACTATGTAATATATATGT 359
OY 868 agtcc 872
|||||
DB 360 AGTCC 364

RESULT 6
AA394359 534 bp mRNA EST 30-OCT-1997
LOCUS 25942 Lambda-PR2 Arabidopsis thaliana cDNA clone 305G17 3', mRNA
DEFINITION
AA394359
VERSION
AA394359.1 GI:2047570
KEYWORDS
EST.
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euhylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
1 (bases 1 to 534)
Newman,T., deBruin,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Onltogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
JOURNAL
MEDLINE
COMMENT
On May 18, 1995 this sequence version replaced gi:811121.
Contact: Thomas Newman

MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313cne@dm.cl.msu.edu
Seq primer: 77.

FEATURES

source

Location/Qualifiers

1..534
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="305G17"

/note="Vector: lambda Zip-lox; Site_1: Sal; Site_2: Not;
lambda PR2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRU's lambda Zip-lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA. " 18 others

BASE COUNT 151 a 114 c 125 g 126 t

ORIGIN

Query Match 31.7%; Score 336.8; DB 33; Length 534;
Best Local Similarity 85.1%; Pred. No. 2.8e-75;
Matches 404; Conservative 0; Mismatches 62; Indels 9; Gaps 3;

OY 467 tgaagtgtatctgtacaacaactctacagggatagttccactcttgggaaat 526
|||||
DB 1 TCAGCTTGATCTGTACAAACAAATCTTACAGGATGTTCCCACTCTTGGGAAAT 60
OY 527 tgaagtctgtctcttcttaagcgttaatgaacacgattgaagggtccatccctagag 586
|||||
DB 61 TGAAGCTCTGTGCTTTTATGCGCTTAATGACAAACGATGACCGTCAATCCCTGAG 120
OY 587 caactcactcaatcccaagccttaagttgtgtatgtctcaagaatgattgtgaa 646
|||||
DB 121 CACTACGGCAATCCCAAGCCTTAAAGTTGTGACGTCTCAAGCAATATTTGTGTGAA 180
OY 647 caatcccaacaaacgacattgtctcaatcccttacaagaacttgaagaacaccga 706
|||||
DB 181 CAATCCCAACAAACGACCTTGTCTCAATCTTACAGAACTTGAGAAACCCGA 240
OY 707 ggttggagggacgggaattactcgttcttgaagtaagaacactacgcctgaaaaa 766
|||||
DB 241 GATTGGAGGACCGGAATTAATGCTTTCGCAAGCTAGACATCACTAGNANCGAAACA 300
OY 767 attggcaaacctgaaatgaagaattggggggtg---accitglaagaacattcacca 823
|||||
DB 301 ACTGGCAAAACCTGGAATGAGNATTTGGGGGGGTGACCTTTGAAGNACACTTCANCA 360
OY 824 cttatcaaatatcacatctac---tatgtaataagtatatatgtgattccaaa---aa 877
|||||
DB 361 CATTATCCAAATATCCATCATTAANGNATNATGATATATGATGNGTAAACCAA 420
OY 878 aaaaatgaagaatgaatcagtaataatcatctgtctcaatttgaagattggag 932
|||||
DB 421 AAAAATTGGGGATCCGATCGGGAANANANCGGGGCCCAATTGGGAACTNGNGGG 475

RESULT 7
A1100682 348 bp mRNA EST 21-AUG-1998
LOCUS 33803 Lambda-PR2 Arabidopsis thaliana cDNA clone 105L1XP 3', mRNA
DEFINITION
A1100682
VERSION
A1100682.1 GI:3449392

KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 348)
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL Plant Physiol. 106, 1241-1255 (1994)
MEDLINE 95148729
COMMENT On May 5, 1995 this sequence version replaced g1:797667.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@lhm.cl.msu.edu
The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation.
Seq primer: M13-21.

FEATURES
Location/Qualifiers
1..348
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="185LXP"
/note="Vector: lambda Zip-Lox; Site.1: Sal; Site.2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRU's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."

BASE COUNT 110 a 74 c 66 g 93 t 5 others
ORIGIN

Query Match 31.28; Score 332; DB 42; Length 348;
Best Local Similarity 99.1%; Pred. No. 4.5e-74;
Matches 332; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 538 gtcttttaagcgttaagacaacgattgacggcgccaactcctaagcactacgca 597
|||
Db 14 gctcttttACGCTTAAGACACCGATGACGGGCCAATCCTTAGACACTACCTGCA 73

Oy 598 atcccaagccttaagatgtgtgatgtctcaagcaatgatgtgtggaacatccaca 657
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Db 74 ATCCCAAGCCTTAAGATGTTGATGATCTCAAGCAATGATTTGTGTGAACAATGCCACA 133

Oy 658 aacggaccttctgcacatctccttaacagaacttgaagaacacccgaagttggagga 717
|||
Db 134 AACGCACTTTGCTCACATCTCTTACAGAACTTGAAGAACACCCGAGTTGAGAGGA 193

Oy 718 ccgaataaccgcgtcttgcaagctacgaacactacgacactgaaaaattggcaaac 777
|||
Db 194 CCGGATTAACCTGAGTCTGCAAGCTACGACACTGACACTGAAAAAATGGCAAAAC 253

Oy 778 ctgaataatgaagaacttggggggtgacctgtgaagaacactccacacattatcaaatc 837
|||
Db 254 CTGAATAATGAAGAATGGGGGGTGANCTGTGAAGAACACTTCACACTTTATCAAAATATC 313

Oy 838 aacatcactatgtaataagatatatatatgtagtcc 872

Db 314 AACTCTACTATGTATTAAGTATATATGTAATGCTCC 348
|||||

RESULT 8
AA712221
LOCUS
DEFINITION
AA712221 401 bp mRNA EST 24-DEC-1997
31949 Lambda-PRL2 Arabidopsis thaliana cDNA clone 180C977, mRNA sequence.
ACCESSION
VERSION
AA712221.1 GI:2722138
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 401)
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL Plant Physiol. 106, 1241-1255 (1994)
MEDLINE 95148729
COMMENT On Sep 19, 1997 this sequence version replaced g1:1520373.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@lhm.cl.msu.edu
Seq primer: T7 dye primer.

FEATURES
Location/Qualifiers
1..401
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="180C977"
/note="Vector: lambda Zip-Lox; Site.1: Sal; Site.2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRU's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."

BASE COUNT 103 a 105 c 78 g 99 t 16 others
ORIGIN

Query Match 31.0%; Score 329.2; DB 37; Length 401;
Best Local Similarity 89.8%; Pred. No. 2.3e-73;
Matches 354; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

Oy 85 ctgcacctcgcagatgacatggcgtctcgaaacatcggtggagctcttcgcagct 144
|||
Db 1 CTTAAACNCMGCAAGAGCTCATGCGCTCGAAACCTATCGGTGGAGACTCTTGGCACT 60

Oy 145 tggtaataacctagacttgtagcttaacctggtcggaagaaactcggaagagatgct 204
|||
Db 61 TCGTTAACCTTAACCTTACTTATATCAACNGTGAAGCAACNCGGAAGANATNCT 120

Oy 205 cttaagctcttcgcgcgaggtttaacagatccggaacatgtctccagagctggatcca 264
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Db 121 CTCTAGCGCTCTTGGCGGAGTTTGAACAGATCCAGACCAATGTCCTCCAGAGCTGGGATCCA 180

QY	265	acctgttcaatccctgtacacccgtgtccatcttcaacccaagaacccgctacat	324
Db	181	ACINTHTSTNAATCTCTGTACCGNGTTCATATGTNACCTCTAACAAGAACCCGCTCACT	240
QY	325	ctgtgtgatttgggggaattcaaacctctctgacatctctggcctgtgacttgggaacct	384
Db	241	CGTGTGATTTTGGGAATTTCAACANNCTCTGGACATCTTGCGNCTGAGCTTGGGAAGCTT	300
QY	385	gaacatttcagatcttagagctctcaaaaacaaacccaagaacttaaccttcgga	444
Db	301	GAACATTTCAGATCTTAGAGCTCTTACCAAAACCAACCATCAAGACTATACNTCCGAA	360
QY	445	cttggaaattcgaagaatctcatcagcttggatc	478
Db	361	CTTGGAAATCTGAAG-ATCTCATCAAGNTTGGATC	393
RESULT	9		
LOCUS	H37300	353 bp	MRNA
DEFINITION	15429 Lambda-PRL2 Arabidopsis thaliana cDNA clone 179J1977, MRNA sequence.		EST
ACCESSION	H37300		30-DEC-1997
VERSION	H37300.1	GI:906799	
KEYWORDS	EST.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 353)		
AUTHORS	Newman,T., debruin,F.J., Green,P., Keegstra,K., Kende,H., McInosh,L., Ohlroge,J., Ratkbel,N., Somerville,S., Thomasow,M., Retzel,E. and Somerville,C.		
TITLE	Gene galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)		
JOURNAL	5146729		
MEDLINE	On May 8, 1995 this sequence version replaced g1:801146.		
COMMENT	Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PR, Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 223j3tce@dm.c1.msu.edu Seq primer: T7 dye primer.		
FEATURES			
source	1..353		
	/organism="Arabidopsis thaliana"		
	/strain="var columbia"		
	/db_xref="taxon:3702"		
	/clone="179J197"		
	/clone.lib="Lambda-PRL2"		
	/note="Vector: lambda zip-lox. site.1: Sal; site.2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."		
BASE COUNT	98 a	85 c	67 g 89 t 14 others
ORIGIN			
Query Match	30.8%	Score 327.8;	DB 23; Length 353;
Best Local Similarity	94.1%;	Pred. No. 5.2e-73;	
Matches 333; Conservative	0;	Mismatches 21;	Indels 0; Gaps 0;

REFERENCE	TITLE	JOURNAL	COMMENT
409	1 (bases 1 to 608)		
409	D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Hansen, T.S., Rohning, C.M., Craven, M.B., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.		
409	Generation of ESTs from tomato callus (mixed elicitor)		
409	Unpublished (1999)		
409	On Dec 20, 1995 this sequence version replaced gi:1135853.		
409	Contact: David Fritsch		
409	Clemson University Genomics Institute		
409	100 Jordan Hall, Clemson, SC 29634, USA		
409	Tel: 864 656 4366		
409	Fax: 864 656 4293		
409	Email: dfritsch@CLEMSON.EDU		
409	5 prime sequence.		
409	Location/Qualifiers		
409	1. 608		
409	/organism="Lycopersicon esculentum"		
409	/cultivar="Rio Grande Ptor"		
409	/db_xref="taxon:4081"		
409	/clone="cLEM43M10"		
409	/clone.lib="tomato mixed elicitor, Bt1"		
409	/tissue_type="leaf"		
409	/dev_stage="4-6 week old plants"		
409	/lab_host="XLI-Blue MRF"		
409	/note="Vector: pBluescript SK(-); site_1: EcoRI; site_2: XhoI; cLEM - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BtH, jasmonic acid, ethylene, fenchone, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."		
409	BASE COUNT		
409	165 a 126 c 134 g 183 t		

REFERENCE	Arabiidopsis. 1 (bases 1 to 339) Newman,T., deBruin,J., Green,P., Keegstra,R., Kende,H., McIntosh,L., Ohlrogge,J., Ralphe,J., Somerville,S., Thomashow,M., Reisel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1253 (1994) 95148729
JOURNAL MEDLINE	On May 5, 1995 this sequence version replaced gi.797664. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313rcn@lsm.c1.msu.edu
COMMENT	The sequence entry for this EST has been reverse complemented and is being submitted in the sense orientation. Seq primer: M13-21.

RESULT	13
H36800	
LOCUS	
DEFINITION	H36800 447 bp mRNA EST 30-DEC-1997 14929 lambda-PRL2 Arabidopsis thaliana cDNA clone I79A22T7, mRNA sequence.
ACCESSION	H36800
VERSION	H36800.1 GI:906299
KEYWORDS	EST.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 447) Newman,T., DeBrujin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
JOURNAL MEDLINE	95148729
COMMENT	Contact: Thomas Newman

	Query Match	29.6%	Score 314.6;	DB 42;	Length 339;	
	Best Local Similarity	97.0%;	Pred. No. 1.2e-69;			
	Matches 328; Conservative	0;	Mismatches 9;	Indels 1;	Gaps	1;
QY	536 tggctttttaagcgttaatgacaacgcgatltacgaggccaa-tccctagcactact	594				
Db	2 TGTCTTTTATTAGGCTTAATGACAACCGATTACGGGGCAATTCCTTAGACACTCACT	61				
QY	595 gcaatcccgaagccttaaagtgttgatgctcaagaacatgatltylbgynaacatccca	654				
Db	62 GCATTCCCAAGCCTTAAGTTGTGATNTCTCAAGCAATGATTTGGTGGAACANTGCCA	121				
QY	655 aaaaacgagaccttggctcacatctccttaacgaactttgaaaaaacaccggguttggag	714				
Db	122 ACAAAAGGACCTTTTGCTGCATCTCCCTTTACAGAACTTTGGAACACAACCAGGTTGGAG	181				
QY	715 gagaccggaattactcgcttcgacgactacgacactaactgcactgcgaaaaattggcaa	774				
Db	182 GACCGGGAATTACTCGGGCTTCGAAAGCTACGACACTCACTGCACCTGAAAAAATTGGCAA	241				
QY	775 aaactgaaaaatgaagaattgggggyltgacctlytgaagaacacttcaccaattatcaaat	834				
Db	242 AANCTGAANAATGAGAAGATTGGGGGGTGACCTTGTAGAAGACACTTCACACTTAGCAAT	301				
QY	835 atcacactcactatgyataataagtatatatatatgatgcc	872				
Db	302 ANCACTTACTCATGTAAATGAATAATATATATATAGMCC	339				

	BASE COUNT	106 a	115 c	83 g	126 t	17 others
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Query Match	28.4%;					
Best Local Similarity	86.9%;					
Matches	371;					
Conservative	0;					
Mismatches	43;					
Indels	13;					
Gaps	4;					
QY	14	ccgaagaaacccaatttgccttcctcacc-ctgttcagaaat-----actca	62			
DB	22	CCAAGTAACCTTAATTTNCTTTCGCCCTTTGTTCAAAATTTCCCTTTACACTCA	81			
QY	63	aattccattagattactctctcttcgcacctcgagatgcacatgsgtctogaaacta	122			
DB	82	AATTCCTTTTCATTTCCCTCTCTTAACACNCGGAAAGCTACATGSGCTCGAAACTA	141			
QY	123	tccgttggagctcttcgcagcttcgtttaaactcctaacttagctttgattcacactgtgcga	182			
DB	142	TCCGTGGGAGCTCTTCGCAGCTTCGTTAACCTTAACCTTAGCTTTGATTACACCGGTGCA	201			
QY	183	agcaaacctccgaagagagatgctcttaagctcttcgcggaggttaaacgactccggaca	242			
DB	202	ACCAAACTCCGAAAGA-NNGCTCTACACCTCTTCGCGGAGTTTACAGATCCAGACCA	260			

	Query Match	29.6%	Score 314.6;	DB 42;	Length 339;	
	Best Local Similarity	97.0%;	Pred. No. 1.2e-69;			
	Matches 328; Conservative	0;	Mismatches 9;	Indels 1;	Gaps	1;
QY	536 tggctttttaagcgttaatgacaacgcgatltacgaggccaa-tccctagcactact	594				
Db	2 TGTCTTTTATTAGGCTTAATGACAACCGATTACGGGCCAATTCCTTAGACACTCACT	61				
QY	595 gcaatcccgaagccttaaagtgttgatgctcaagaacatgatltgtlytgyaaacaatccca	654				
Db	62 GCATTCCCAAGCCTTAAGTGTTGATATNTCTCAAGCAATGATTTGGTGAACANTMCCA	121				
QY	655 aaaaacgagaccttttgtctacacattcccttaacgaactttgaaagaaaccgggutttygag	714				
Db	122 ACAAAACGGACCTTTTGCTGCATCTCCCTTTACAGAACTTTTGAAACACAACCCGAGGTTGGAG	181				
QY	715 gagaccggaattactcgcttcgacgactacgacactaaccttagcactgaaaaaatbgcaa	774				
Db	182 GACACGGGAATTACTCGGGCTTCGAAACCTTCGACACTCACTGCACCTGAAAAAATTGGCAA	241				
QY	775 aaactlgaaaaatgaagatlygggygtlygacctlytgaagaaaccttcaaccaattatcoaat	834				
Db	242 AANCTGAANAATGAGAAGATTGGGGGGTGACCTTGTAGAACACTTCACACTTAGCAAAAT	301				
QY	835 atcacactcactcatgtaataagaatatatatatgatgtcc	872				
Db	302 ANCACATCTACTCATGTAAATGAATAATATATATATAGNCC	339				

	BASE COUNT	106 a	115 c	83 g	126 t	17 others
ORIGIN						
Query Match	28.4%;					
Best Local Similarity	86.9%;					
Matches	371;					
Conservative	0;					
Mismatches	43;					
Indels	13;					
Gaps	4;					
QY	14	ccgaagaaacccaatttgccttcctcacc-ctgttcagaaat-----actca	62			
DB	22	CCAAGTAACCTTAATTTNCTTTCGCCCTTTGTTCAAAATTTCCCTTTACACTCA	81			
QY	63	aattccattagattactctctcttcgcacctcgagatgcacatgsgtctogaaacta	122			
DB	82	AATTCCTTTTCATTTCCCTCTCTTAACACNCGGAAAGCTACATGSGCTCGAAACTA	141			
QY	123	tccgttggagctcttcgcagcttcgtttaaactcctaacttagctttgattcacactgtgcga	182			
DB	142	TCCGTGGGAGCTCTTCGCAGCTTCGTTAACCTTAACCTTAGCTTTGATTACACCGGTGCA	201			
QY	183	agcaaacctccgaagagagatgctcttaagctcttcgcggaggttaaacgactccggaca	242			
DB	202	ACCAAACTCCGAAAGA-NNGCTCTACACCTCTTCGCGGAGTTTACAGATCCAGACCA	260			


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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(512..3149, 3993..4393)
OTHER INFORMATION: /product= "RRK-B"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRR-B from rice (Oryza
US-08-475-891A-3

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Query Match          6.0%; Score 63.6; DB 3; Length 5992;
Best Local Similarity 50.3%; Pred. No. 6.7e-10;
Matches 156; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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```

QY 346 aacctctcgtgacatcttcgacctgagcttgggaagcttgaacattacagatctagag 405
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DB 1670 AAGTTCACAGAGAGCATTCGAGGATATGCGCAATCTTATTTGGCTTACACATCTCTAT 1729

QY 406 ctctacaaacacacacacacacacacacacacacacacacacacacacacacacacac 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1730 CTCTGCAACACATTTTCAAGGCTCTCTTCATCATCGTTGAGGCGCTTAATAAACTTA 1789

QY 466 atcagcttgatctgtacaacacacacacacacacacacacacacacacacacacacac 525
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DB 1790 GGCATTTACTCGGCTTACGAAACAACTTGAGCGGTTGATCCGTTGGCATAGGAAAT 1849

QY 526 ttgaagctctgtctctttaaagcttaataagacacacacacacacacacacacacacac 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1850 CTTACTGAACTTAAATTAATCTTACGCTGCGACACAAATTCAGTGTGGATACCATAC 1909

QY 586 gcactacacacacacacacacacacacacacacacacacacacacacacacacacacac 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1910 ACACCTGCAACCTCAACAACTTGTGTCTATTTAGGCTTTCACTAATACCTTAATGCT 1969

QY 646 acaatcccaa 655
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DB 1970 CCAATACCCA 1979

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RESULT 4
US-08-238-163-3
; Sequence 3, Application US/08238163
; Patent No. 5569830
; GENERAL INFORMATION:
; APPLICANT: BENNETT, Alan
; APPLICANT: LABAVITCH, John M.
; APPLICANT: POWELL, Ann
; APPLICANT: STOLTZ, Henrik

```

```

TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 421..1401
US-08-238-163-3

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Query Match          5.5%; Score 58; DB 1; Length 2075;
Best Local Similarity 50.5%; Pred. No. 2e-08;
Matches 196; Conservative 0; Mismatches 185; Indels 7; Gaps 2;

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QY 269 ttgttaatcccttgaactcgtgttgcattgtaacacacacacacacacacacacacacac 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 576 TTGCTGTTACTGTAAGTATTAATGATGACCGAAAC----CAACGGATTAATGCTC 631

QY 329 tggatttgggaattcaaacctctctggaacacacacacacacacacacacacacacacac 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 632 TCACCGTCTTCCAGCAAGCAATATCTCGGCAAAATTCGCGACCGGTGAGACCTTCAT 691

QY 389 attacagatctagagctctacaaa---aaacacacacacacacacacacacacacacacac 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 692 ATCTCGAATACTTGAATTTTCATATCTTACTTAATCTCACCGAACAATTCACCTGCAA 751

QY 446 ttggaatcttaagaatcctacacacacacacacacacacacacacacacacacacacacac 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 752 TTGGAAGCTTCAAAATCTCAAAATGTTAAGGCTCAAGCTTCACTAATCTTACAGGTCGA 811

QY 506 ttcccaactcttgggaataatggaagctctgtgctctttaaagcttaatggaacacacacac 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 812 TCCCTGAATTCCTTATGCTAGCTGAGTGAAGAAATTTGACGTTGCTGAGATTGAATCAATCAAT 871

QY 566 tgaacgggacacacacacacacacacacacacacacacacacacacacacacacacacacac 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 872 TTACCGAACAATCTCTTCTTCCTCTCTACGCTTCGGAATTTGCTAGAGATGACTTAG 931

QY 626 caagcaatgatattgttggaaacacacacacacacacacacacacacacacacacacacac 653
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DB 932 ATCGTAACAACCTCACCGGAACAATACC 959

```

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RESULT 5

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```

US-08-587-680A-24
: Sequence 24, Application US/08587680A
: Patent No. 5977434
:
: GENERAL INFORMATION:
: APPLICANT: Ronald, Pamela C.
: APPLICANT: Wang, Guo-Liang
: APPLICANT: Song, Wen-Yuang
: APPLICANT: Szabo, Veronique
: TITLE OF INVENTION: Procedures and Materials for Conferring
: TITLE OF INVENTION: Disease Resistance in Plants
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: City: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/587,680A
: FILING DATE: 17-JAN-1996
: CLASSIFICATION: 800
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,375
: FILING DATE: 17-JAN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/475,891
: FILING DATE: 07-JUN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/004,645
: FILING DATE: 29-SEP-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/567,375
: FILING DATE: 04-DEC-1995
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 023070-058940US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1554 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA (partial)
US-08-587-680A-24

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	Query Match	5.28;	Score 55.8;	DB 4;	Length 1554;
	Best Local Similarity	49.58;	Pred. No. 8.4e-08;		
	Matches 144;	Conservative	0;	Mismatches 147;	Indels 0;
				Gaps	0;
QY	348	cctctctgacacctctgcgcctgaagcttggagaagcttgaacaattacagatctagaagct	407		
Db	18	CTTCTGTGGTGACCTTCCTAGTGCATTTAGGAACATATTCAGGCGCTGAAGAATCTGTGGTT	77		
QY	408	ctcaaaaaaacacatccaaggaactatacccttcggaacttggaaatctgaaagatctcat	467		
Db	78	AACGTGAAAAGGTTTCTCAGGTGATATCCCTTCTATTTGGCAGACTAAAGACACATCTT	137		
QY	468	cagcttggatctgttacacaacacacttcacaggaagtgtcccaactcttgggaaaat	527		
Db	138	AAAGCTGGACCTTAGTAGAACAACATCTCTGTGGCAATCCCTCTCAGATGGTAACTG	197		
QY	528	gaagctctcgtctcttttacaggttaatgacaaccgattgacggggccaatccctagac	587		

[illegible]

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RESULT      6
US-08-238-163-1
: Sequence 1, Application US/08238163
: Patent NO. 5569830
: GENERAL INFORMATION:
:   APPLICANT: BENNETT, Alan
:   APPLICANT: LABAVITCH, John M.
:   APPLICANT: POWELL, Ann
:   APPLICANT: STOTZ, Henrik
:   TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
:   NUMBER OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
:   NUMBER OF SEQUENCES: 24
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Townsend and Townsend Hourie and Crew
:     STREET: Stewart Street Tower, One Market Plaza
:     CITY: San Francisco
:     STATE: California
:     COUNTRY: US
:     ZIP: 94105-1493
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: PatentIn Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/238,163
:     FILING DATE: 03-MAY-1994
:     CLASSIFICATION: 800
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Bastian, Kevin L.
:     REGISTRATION NUMBER: 34,774
:     REFERENCE/DOCKET NUMBER: 2307E-540
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (415) 543-9600
:     TELEFAX: (415) 543-5043
:   INFORMATION FOR SEQ ID NO: 1:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 1058 base pairs
:       TYPE: nucleic acid
:       STRANDEDNESS: single
:       TOPOLOGY: linear
:     MOLECULE TYPE: cDNA
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: 34..1023
:   FEATURE:
:     NAME/KEY: misc_feature
:     LOCATION: 1..1058
:   OTHER INFORMATION: /standard_name="Pear PGIP cDNA"
: US-08-238-163-1

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	Query Match	5.2%	Score 55.4	DB 1	Length 1058
	Best Local Similarity	51.4%	Pred. No. 9e-08		
	Matches 128	Conservative	0	Mismatches 121	Indels 0
				Gaps	0
QY	339	gaattcaaacctctcggacatcttcgcgcttgagcttggagaacttgaacattcaagta	398		
DB	342	GCAACCCAAATCTCACTGGGCCAATCCAAACCCGCAATTGCCAAGCTCAAAAGAGCTCAAGTC	401		
QY	399	tctagagctctacaacaaacacatccaaaggaactacatacttcggaacttggaaattgaa	458		
DB	402	TCTCAGGCTCAGCTGGACCAACCTCTCAAGGCTCTGTCCCTGACTTCTCTCAGCCAACTCAA	461		
QY	459	gaatcatcatcagcttggatctcttgaacacacaaattcttcagggatgattccactcttt	518		


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FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease"
OTHER INFORMATION: resistance gene RRK-F from rice
OTHER INFORMATION: (Oryza sativa)"
US-08-567-375-1

Query Match 5.2%; Score 55.4; DB 4; Length 6256;
Best Local Similarity 50.2%; Pred. No. 2.4e-07;
Matches 165; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

OY 329 tggatttgggaattcaaacctctcttgacacattgcgctgagcttgggaagcttgaac 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2735 tggacttgggagaaatAACCTGGGGGAGGCTTCTTCCTAAATTCGTTTCCACTTTTCCA 2794

OY 389 att---taagatctagaagctctacaaaacatcccaaggaactatattccgaac 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2795 CTTCGCTTAGTTTCTTCCACTTGTGTAATAGATACAGAGCAATTCCTCAAGGATA 2854

OY 446 ttggaatctgaagaatctcatcagcttgatctgtacacaacaatcttaaggagtag 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2855 TTGGCAATCTTATGCGTTACACATCTCTATCTCTGCAACACAAATTTGAGGGGTAC 2914

OY 506 ttccactctttgggaagaattgaagctctgtcttcttttcgagcttaagacaacgat 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2915 TTCCATCATCGTTGGGCGAGGCTTAGAATAGGCAATCTAGTCCCTACCAAAACAAC 2974

OY 566 tgaaggggccaatccctagagcactcactgcgaatcccaagcttaagttgtatgct 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2975 TGAGCGGTTGCATCCCATTTGCCATTTGCCATAGCAATCTTACTGAATTAATCTTACTG 3034

OY 626 caagcaatgatctgtgtgaacaatccca 654
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DB 3035 GCACCAACAATTCAGTGTGATACCA 3063

RESULT 9
US-08-587-680A-1
Sequence 1, Application US/08587680A
Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Confering
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Elgth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-0589400S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease"
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
OTHER INFORMATION: sativa)"
US-08-587-680A-1

Query Match 5.2%; Score 55.4; DB 4; Length 6256;
Best Local Similarity 50.2%; Pred. No. 2.4e-07;
Matches 165; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

OY 329 tggatttgggaattcaaacctctcttgacacattgcgctgagcttgggaagcttgaac 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2735 tggacttgggagaaatAACCTGGGGGAGGCTTCTTCCTAAATTCGTTTCCACTTTTCCA 2794

OY 389 att---taagatctagaagctctacaaaacatcccaaggaactatattccgaac 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2795 CTTCGCTTAGTTTCTTCCACTTGTGTAATAGATACAGAGCAATTCCTCAAGGATA 2854

OY 446 ttggaatctgaagaatctcatcagcttgatctgtacacaacaatcttaaggagtag 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2855 TTGGCAATCTTATGCGTTACACATCTCTATCTCTGCAACACAAATTTGAGGGGTAC 2914

OY 506 ttccactctttgggaagaattgaagctctgtcttcttttcgagcttaagacaacgat 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2915 TTCCATCATCGTTGGGCGAGGCTTAGAATAGGCAATCTAGTCCCTACCAAAACAAC 2974

OY 566 tgaaggggccaatccctagagcactcactgcgaatcccaagcttaagttgtatgct 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2975 TGAGCGGTTGCATCCCATTTGCCATTTGCCATAGCAATCTTACTGAATTAATCTTACTG 3034

OY 626 caagcaatgatctgtgtgaacaatccca 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3035 GCACCAACAATTCAGTGTGATACCA 3063

RESULT 10
US-08-473-553A-1
Sequence 1, Application US/08473553A
Patent No. 5859338
GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
```


Db 2973 TGGACCTTCGATGCTGATCTGTCTCAACATGCTTGGAAAGGTCATATACCGCATCATTT 3032
QY 519 gggaaatgaagctctgctgtcttttaagcgttaagcaaccgagatgagggccaat 578
Db 3033 TCATAATTATACATGACTGACGAACTTTGGATCTCTCATCTAATAATACGCGAGAAAT 3092
QY 579 ccctaagagcactcactgcaatcccaagccttaagtgctgtagctcaagcaatgatt 638
Db 3093 TCCCGACGACGCTTCGATCCCTCACATTCCTTGAAGTCTTAATCTCTCCCATCATCT 3152
QY 639 gtgtggaacaatcccaacaacgacctttgct 672
Db 3153 TGTGTGATGATCCCAAGAAACAATTGGAT 3186

RESULT 14
US-08-244-646-14
; Sequence 14, Application US/08244646
; Patent No. 5744692
; GENERAL INFORMATION:
; APPLICANT: Cervone, Felice
; APPLICANT: De Lorenzo, Giulia
; APPLICANT: Salvi, Giovanni
; APPLICANT: Albersheim, Peter
; APPLICANT: Darvill, Alan
; APPLICANT: Bergmann, Carl
; TITLE OF INVENTION: Nucleotide Sequences Coding An
; TITLE OF INVENTION: Endopolygalacturonase Inhibitor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sally A. Sullivan
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,646
; FILING DATE: 06-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT RM 91A 000915
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IT/00158
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 19-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Phaseolus vulgaris
; STRAIN: Saxa
; IMMEDIATE SOURCE:
; CLONE: lambda PGIP-3.3

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1026
; FEATURE:
; NAME/KEY: 3' UTR
; LOCATION: 1027..1116
US-08-244-646-14

Query Match 3.9%; Score 41.4; DB 2; Length 1116;
Best Local Similarity 48.1%; Pred. No. 0.0021;
Matches 117; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 411 caaaacaacatccaaggaactatacctccgaacttggaaatcgaagaatcgaag 470
Db 342 CATCAATACCTGTCGTCGATCCCGCCGCAATACCGATTCTTGTACAGATCA 401
QY 471 ctggatctgtacacaacatcttacagggatagttccactcttgggaaatgaa 530
Db 402 TCTCTATATGACTGACACCAATGTCTCCGCGCAATACCGATTCTTGTACAGATCA 461
QY 531 gctctgtcttttaagcgttaagcaaccgattgaagggccaatccctagagact 590
Db 462 AACCTCGTACACCTCGACTTCTCTACACGCGCTCTCGGACCGCTCCCTCCAT 521
QY 591 cactgcaatcccaagccttaagtgctgtagctcaagcaatgattgtgtgaaat 650
Db 522 CTTCTCTCCCAACCTGCGGAGATCAATTCAGCGCAACCGAATCTCCGCGCAT 581
QY 651 CCC 653
Db 582 CCC 584

RESULT 15
US-08-592-936B-20
; Sequence 20, Application US/08592936B
; Patent No. 5783393
; GENERAL INFORMATION:
; APPLICANT: Kellogg, Jill A.
; APPLICANT: Bestwick, Richard K.
; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
; TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,936B
; FILING DATE: 29-JAN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4257-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear

[illegible]

QY	361	atctcttgcaatggttccatgctacgttcaacaacagagaaacgtgtctataagtgatttc	420
Db	361	ATCCTTGCAACATGGTTCCATGTCACCTTGGACAACAACAGAAACAGTGTCTAAAGAGTGAATT	420
QY	421	tgggaatgacgaattatctcggccattagttccagacttggtgtgtccaaagattctgc	480
Db	421	TGGGAATGCAAGATTTATCTGGCCATTAGTTCACAGCTTGGTGTGCTCAAGAATTGGC	480
QY	481	agatcttgagctttacagtaacaacaaactagtcgccgatctccatglaactcttgaaac	540
Db	481	AGATTTTGGAGCTTTACAGTAAACAATAACATGGCCCGCATTCCTGTGATCTTGGAAATC	540
QY	541	tgcacaacttagtgaaatttgatcttacttaaaagctctccgagctctcttcocgagat	600
Db	541	TGCACAACCTTAGTGAAATTGGAATCTTTACTTAAACAGCTTCTCCGGTCTATTCCGGAAT	600
QY	601	catitggagaacgtttcaaacgttgaatttctccgggtttacaacaacagttcactgagt	660
Db	601	CATTGGGAACCTTTCAAACTGTGATTTCTCCGGTTAAACAACAAGTCTCACTGGGT	660
QY	661	caattctatgtactgacccaatatattacaccttaagtgttaagtattacaataaca	720
Db	661	CAATTCTATGTACTGACCCAATATTATACCTCTTAAGTGTAAATGATCAATAATAACA	720
QY	721	gactctctgtctacgtctccctgacaatggtctctctcactctcacaaccactagtttg	780
Db	721	GACTCTGTGTTGAGTTGCGACAAAGGGTCCTGTCACTCTTCAACACCACATCAAGTTTG	780
QY	781	ctaataacttagacctatgtggaacgtgttacaagtacccaatgctctgtactccccgt	840
Db	781	CTAATAACTTAGACCTATGTGGACGCTGTAAACAAGTACCCAAAGTCTGTGATCTCCCGGT	840
QY	841	ttctcccccacaaccccttattacaacctccccagtttccaaaccggagtgtgata	900
Db	841	TTTCTCCCTCCACACCTTTATTCACACTCCCAATTTCCACCCGAGTGGATGGTA	900
QY	901	taactggaagcaatagctgtgtgagattgtgtcgaaagtgtcgtcttgcccttgctgtc	960
Db	901	TAACTGGAGCAATAGCTGTGGAGATGTGCTGACAGTCTCTTTGGCCCTTGTGCTGCTCG	960
QY	961	caatagcccttgcgttgtgtgcgaacgaagagcccaatagatatcttctctgagtccgt	1020
Db	961	CAATAGCCTTGTGCTGTGTGGCGACGAAGAAAGCCCACTAATATTTTCTTCATGTCCCTG	1020
QY	1021	cogaagaagaatccagaagttcatctctggagagctcaagaagttctcttgcggagctac	1080
Db	1021	CGAAGAAGATCCAGAAAGTTCACTGTGGACAGCTCAAGAGGTTTCTTTGCGGAGCTAC	1080
QY	1081	aagtggtgagtgatgggttttagtaaaagaacatttgggcagagtggtgtttggaag	1140
Db	1081	AAGTGGCAGTGAAGGGTTTAGTAAACAAGAACATTTTGGCGACAGAGTGGGTTTGGGAAG	1140
QY	1141	ctctacaagggacgtcttgcagacgagactctgtgtctcaagaagacttgaaagaagc	1200
Db	1141	CTCTACAAGGACGCTTGGCAGACGGAACCTCTGTCTCAAGAAGACTGAAGAAAGAC	1200
QY	1201	gaactccaagtgtgagagctcccaagttccaacagaagttagagatgaatgtatgcagctc	1260
Db	1201	GAACTCCAGGTGGAGACTCTCAGTTTCAACAACAATAAGATGATGAATAGGAGATTC	1260
QY	1261	atcgaaacctttagaattacagagttctcgtatgacacggacggagagatgtctgtgt	1320
Db	1261	ATCGAAACCTTTAGATTAACAGAGTTTCTGTATGACACCGAACGAGATTTGCTTGCT	1320
QY	1321	atcccttacaatgccaatgaaagtgtgtgtcgtgtctcagagagaagccacgcgtcaaac	1380
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RESULT 2
LOCUS DCU93048 1755 bp mRNA PLN 28-JUN-1997
DEFINITION Daucus carota somatic embryogenesis receptor-like kinase mRNA,
complete cds.
ACCESSION U93048
VERSION U93048.1 GI:2224910
KEYWORDS .
SOURCE carrot.
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
REFERENCE 1 (bases 1 to 1755)
AUTHORS Schmidt,E.D., Guzzo,F., Toonen,M.A. and de Vries,S.C.
TITLE A leucine-rich repeat containing receptor-like kinase marks somatic
Plant cells competent to form embryos
JOURNAL Development 124 (10), 2049-2062 (1997)
MEDLINE 97313247
JOURNAL 2 (bases 1 to 1755)
REFERENCE Schmidt,E.D., Guzzo,F., Toonen,M.A.J. and de Vries,S.C.
AUTHORS Direct Submission
TITLE Submitted (12-MAR-1997) Molecular Biology, Agricultural University
JOURNAL of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands
FEATURES
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LOCUS A67797 1815 bp DNA PAT 05-MAY-1999
DEFINITION Sequence 2 from Patent WO9743427.
ACCESSION A67797
VERSION A67797.1 GI:4756623
KEYWORDS
SOURCE
ORGANISM
Daucus carota
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
REFERENCE
1 (bases 1 to 1815)
De V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.

TITLE PRODUCTION OF AROMATIC SEED
JOURNAL Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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location/Qualifiers
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Query Match 44.7%; Score 934.8; DB 5; Length 1815;
Best Local Similarity 74.5%; Pred. No. 3e-251;
Matches 1192; Conservative 0; Mismatches 402; Indels 6; Gaps 1;
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DEFINITION	Arabidopsis thaliana chromosome 1 BAC F14023		sequence, complete
ACCESSION	ACOL12654.2	GI:6554462	
VERSION			

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SOURCE	thal cress.
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	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE	Arabidopsis.
AUTHORS	1 (bases 1 to 98471)
	Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
TITLE	Toriumi,M., Chin,C., Chou,J.J., Choi,E., Gonzalez,A., Homg,B.,
AUTHORS	Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,S.,
JOURNAL	Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.,
	Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
	Shim,P., Tambunga,G., Davis,R.W., Ecker,U.R., Federspiel,N.A. and
	Theologis,A.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 98471)
AUTHORS	Theologis,A.
TITLE	Direct Submssion
JOURNAL	Submitted (02-NOV-1999) Plant Gene Expression Center, 800 Buchanan
	Street, Albany, CA 94710, USA
REFERENCE	3 (bases 1 to 98471)
AUTHORS	Theologis,A.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-1999) Plant Gene Expression Center, 800 Buchanan
	Street, Albany, CA 94710, USA
COMMENT	On Dec 10, 1999 this sequence version replaced g1:6175131.
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 Db 80638 CAGGACAAAGACCTTTCATCTCGCTCGCTAGCTAACGACGACGCTCATGTTACTTG 80697
 QY 1753 actg----- 1757
 Db 80698 ACTGGGTAATACACATTAACATTCATTTGACCCCAACAAACCATTTGAAACGAGNA 80757
 QY 1757 -----ggtgaaagatctgttgaagagaaagact 1786
 Db 80758 TCTAATCTCAATACTGTTTGTGTTAGTGAAGAGATTGTTGAAGAGAGAAAGCT 80817
 QY 1787 aagatgttagagagatcagatctcacaacacagagagagagagagagagagagagag 1846
 Db 80818 AAGAGATGTAGTGATCCAGATCTTCAACAACTACAGAGAGAGAGAGAGAGAGAGAG 80877
 QY 1847 gataaagatgagcttgcatagcagcaagagatcaccaatggaagacaaagatgctcga 1906
 Db 80878 GATACAGATGGCGTTGCTATGACAGCAAGAGATCACATATGAAAGACCAAGAGTGTG 80937
 QY 1907 aattgttaagagatgctggaagagagatgagctgcggaagaaatggaagacagagagag 1966
 Db 80938 ACTTTGAAGATGCTGGAAGAGAGATGGGCTGCCGGAAGAAAGGCGAATGCAAAAAAGT 80997
 QY 1967 tgaagatttgaagagagagatgatttgaagcttaacttaacttgaatttga 2026
 Db 80998 TGAGATTTGAGAGGAAGAGATTTGATGATCTTAATCTTAATCTGATTTGATTTTGA 81057
 QY 2027 tctacttaacattgcagcgccgtgagctatctgctcgaagtaaaaaa 2086
 Db 81058 TTCTACTTACATTTGACGCGCTTGAAGTATCTGTCCAAAGTAAAAAACAACATA 81117
 QY 2087 aaa 2089
 Db 81118 AAA 81120

RESULT 5
 A67815 4081 bp DNA PAT 05-MAY-1999
 LOCUS A67815
 DEFINITION Sequence 20 from Patent WO9743427.
 ACCESSION A67815
 VERSION A67815.1 GI:4756638
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.
 REFERENCE 1 (bases 1 to 4081)

AUTHORS De V.S., Schmidt E.D., Van H.G. and Hecht, V.F.
 TITLE PRODUCTION OF APOMITIC SEED
 JOURNAL Patent: WO 97/43427-A 20-NOV-1997;
 CIBA GEIGY AG (CH)
 FEATURES
 source Location/Qualifiers
 1..4081
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="ARABIDOPSIS SERK GENE"
 exon 1280..1367
 exon 1796..1928
 exon 2014..2085
 exon 2203..2346
 exon 2450..2521
 exon 2617..2688
 exon 2772..2884
 exon 3015..3146
 exon 3305..3646
 exon 3760..4081
 BASE COUNT 1120 a 770 c 785 g 1406 t
 ORIGIN

Query Match 25.9%; Score 540.8; DB 5; Length 4081;
 Best Local Similarity 85.3%; Pred. No. 1.2e-140;
 Matches 665; Conservative 0; Mismatches 2; Indels 113; Gaps 1;

QY 1018 ctgcggaagaagatcagaagatcctcagcagcagcagcagcagcagcagcagcagcagc 1077
 Db 3302 CAGCCGAAGAAGATCCAGAAGTTCATCTGAGACCTCAAGAGGTTTCTTTCGCGAGC 3361
 QY 1078 tacaagctgcagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 1137
 Db 3362 TACAAGTGGGAGATGATGGTGTATTGAACAGAACATTTTGGCGAGAGGTGGTTGGGA 3421
 QY 1138 aagctcaacaggaagccttgcagacagacagacacacacacacacacacacacacac 1197
 Db 3422 AAGTCTACAGGAGACCTTGGCAGACGAACTTGTGCTGCTCAAGAGCTGAAGGAG 3481
 QY 1198 agcgaactcagctgagagagctccagcttcaacacagagatgagatgagatgagatgag 1257
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 QY 1258 tcaatcgaac 1317
 Db 3542 TGTATGAAACCTGTTGAATTTACGAGGTTTCTGTATGACACCGACGAGATGCTTG 3601
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 QY 1361 ----- 1361
 Db 3662 TTAAACATCTGTGCTCTCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 3721
 QY 1361 -----agaagagccacccgtcaaacctcc 1384
 Db 3722 TTATGGTTCAATATTGTTGTTACATTAATGACACAGAGAGCCACCGTCAACACTCC 3781
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 QY 1445 acatgac 1504
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RESULT 6
F23M19/c 88401 bp DNA PLN 17-JUN-1999
LOCUS Arabidopsis thaliana chromosome 1 BAC F23M19 sequence, complete
DEFINITION sequence.
ACCESSION AC007454
VERSION AC007454.3 GI:5091613
KEYWORDS HTG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;
Arabidopsis.
REFERENCE 1 (bases 1 to 88401)
AUTHORS Vysotskaya,Y.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,
Lee,J., Liu,A., Li,J., Kremetskaya,L., Luros,J., Gonzalez,A.,
Altafi,H., Araujo,R., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,
Hansen,N., Huizari,L., Kim,C., Palm,C., Rowley,D., Shin,P.,
Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A.
Arabidopsis thaliana chromosome 1 BAC F23M19 sequence
Unpublished (1999)
2 (bases 1 to 88401)
AUTHORS Theologis,A.
JOURNAL Direct Submission
Submitted (01-MAY-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 88401)
AUTHORS Theologis,A.
JOURNAL Direct Submission
Submitted (04-JUN-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 88401)
AUTHORS Theologis,A.
JOURNAL Direct Submission
Submitted (17-JUN-1999) Plant Gene Expression Center, 800 Buchanan
St., Albany, CA 94710, USA
COMMENT On Jun 17, 1999 this sequence version replaced gi:4966902.
The sequence of BAC F23M19 from Arabidopsis thaliana chromosome 1.
FEATURES
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GLTSDSSSAIKHLAYDTAKTGNVVISNHRIGGVSYSDCFYNAGWTDTRVAVDY
LQHKYRAPLEIAGTISGANVIAKYVIGEGEGLPVSLGAVAISPMDLIDGRDRIYD
KOKLYKALITIGOGYAOALHEPOFLRLANMEGIIKRSRISRDPDNATCIYGFEPVDT
YKSSSTQYVGNVAVPLICISALDPLCTKRAIPWDECRANKNIYLAITNNGHLAF

PEGLTSSLMWRATNEFLGLVLCSPYMHIOKIVDKRSSGSGKQEPSNOCYPIALAE
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GVAHCSLFQDRKDPKMSKRAKLQNTQKSGPNDPVPVLDQMTPLEVDNQIKQKSO
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MSYVOPMPKINYNNQWVTEMEENITTKTGTNRLRGVTLDPVPVKIDPEIGSEIS
KLTEGKKFGLSOTLRSPTEIONKQSSSRCTKVOQGYATIGRANVSLVNGDOLL
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complement(28888..31377)
/note="Contains similarity to gi|479356 protein kinase PK1
from zea mays, is a member of the PF100954 S-100s
glycoprotein family and contains a PF100069 Eukaryotic
protein kinase domain."

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PLFTDSAKFLIWEFRNMLAGTAKITTLHEECRCIYCHDIPENIILVDNPAKY
SDFLAKLNPKNRKNYNSVRGTGTYLAPWELANLPITKSDIVSYGVANLLELVSK
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EIALSILLVDFGFMRODSKSSNGTSIPRIQHTOVSKDIVIYPTHLPLDLDSO
NORHSILYFKGAHRRHGLIRKIMDLVNEPGVMEGPNATGRROSTRGMS
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Best Local Similarity 65.0%; Pred. No. 8e-119;
Matches 840; Conservative 0; Mismatches 242; Indels 211; Gaps 2;

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Db 73241 TGGGCGAGGTGGGTTCGGAAGAAGCTCAAGAGGCCGCTTGATGAGAACATCTGTTG 73182
QY 1177 cgtctaaagaactgaagaaagcgaactcccaagtggaagagctccagtctcaaaagaag 1236
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Db 73121 TGGAGATGATTAAGCATGGCCGCTTCAAGAAATTCCTCAGGCTACGGGTTCTGTATGA 73062
QY 1297 caacgaacgaagatctgtctgtatccctcaatggccaatggaagtgctgtctgtc 1356
Db 73061 CCCCTACCGAGAGATGCTTGTATCCTTACATGGCTTAAAGAAAGTGGCTTCGCTT 73002
QY 1357 taga----- 1361
Db 73001 TAGAGAGTAACTTGGAAATTTAACTGTTGTATCATTAAGTAAAGAGCTCCACATG 72942
QY 1361 ----- 1361
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QY 1402 ggaagaagatcgcgctgaagctcgaagcttgctcttaacatgaatcgaatcgcgac 1461
Db 72821 GACAGGAATCGCGCTAGAGTACGAGGAGGTTGTCTTATCTTCAATGATCATTCGAC 72762
QY 1462 cgaagatcatcaccgtgacgtaagcgaagcaaacatcccttgagaagaatctggaag 1521
Db 72761 CCAAAATTAATTCACCGCTGATGGAAGCGCTTAAATTTCTTGGACGAGAAATTTAG 72702
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Db 72641 CGGCTGTGGGTGGGCTATTGAGACATTCCTCGATTAATCTTCACTGGAATCTT 72582
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QY 1702 ggccttcgactcgcctcgcgtagctaaacgaacgacgctcaatgcttaactgactg---- 1757
Db 72521 GAGCTTTGATCTTGCAGAACTGCGGAATGACGATGAGCTTATGCTCATATTGGGTAT 72462
QY 1757 ----- 1757
Db 72461 AACACAGATCTTTAGACATATCGCTATCTCTCAAAAAGCTGATTTATCTGTCAAT 72402
QY 1757 -----ggtagaagatctgtgaaggaagcctagagatcttagtgatctca 1805
Db 72401 TGGTCTTCTCAGGTGAAGAGGCTTTTGAAGAGAAAGCTGGAGATCTGTGTGATCT 72342
QY 1806 gatcttcaacaacactcgaagaggaagaaactcgaagaagtatacaagtggcgttgccta 1865
Db 72341 GAGCTCAAGCAAGCAATTAACACAGAACAGAGTAAGTAAGCAATCAAGTGGCTTCTC 72282
QY 1866 tgaacgaagatgaacaaatggaagaaagaaagatgctgaagatgtaagatctgaa 1925
Db 72281 TGCACACAGAGCTCACTTAAGAGACCTTAAGATGTGTGAGTTGTTCGATGCTTGA 72222
QY 1926 ggaagctgggtctgaggaagaaatggaacgaatgcaaaaagtgtgaattcttaggaaag 1985

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Db	72161	GTGAGAGCTCTTCTTACACCCACCTCGACTGACGTGACCTGATTTCGATTCGATGATTCAT	72102
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Db	72101	GCTATGAGATTCTCTGTCACAGATTAACGACA	72059
RESULT 7			
LOCUS	ATF17M5	96475 bp	DNA
DEFINITION	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project).		
ACCESSION	AL035678		
VERSION	AL035678.1	GI:4490291	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 96475) Bevan, M., Rose, M., Hempel, S., Entjan, K.-D., Hohenseil, J., Mewes, H.W., Mannhaupt, G., Mayer, K.F.X. and Schellner, C.		
JOURNAL	2 (bases 1 to 96475) Unpublished		
REFERENCE	EU Arabidopsis sequencing, project.		
AUTHORS	Direct Submission		
TITLE	Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopfersplitz 18a, D-82152 Martinsried, FRG. E-mail: schuellemips@biochem.mpg.de, mayer@mps.biochem.mpg.de		
JOURNAL	Schuellemips biochem.mpg.de, mayer@mps.biochem.mpg.de		
	Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bsrc.ac.uk		
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/ .		
FEATURES	location/Qualifiers		
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VERSION AC006436.4 GI:6598565
KEYWORDS HTG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
REFERENCE 1 (bases 1 to 65899)
AUTHORS Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
Fuji, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,
Felchljum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M.,
Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanden, S.E., Umayan, L.,
Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,
Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,
Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
Venter, J.C.
TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana
NATURE 402 (6763), 761-768 (1999)
20083487
2 (bases 1 to 65899)
Lin, X.
DIRECT SUBMISSION
Submitted (13-DEC-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
ON DEC 17, 1999 this sequence version replaced gi:4726109.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(http://www.tigr.org/tdb/at/at.html).

COMMENT
Genes were identified by a combination of three methods: Gene
prediction programs including GRLIT
(ftp://artur.epm.ornl.gov/pub/xgrail), GeneFinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://genomic.stanford.edu/GENSCAN.html), and NetPlantGene
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were
identified by RepeatMasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
numbered from the top to the bottom of the chromosome.

database support.
This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.
Address all correspondence to: at@tigr.org.

FEATURES
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complete sequence.
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VERSION
AB013395.1 GI:3128142
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HTG.
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Arabidopsis.
REFERENCE
1 (sites)
AUTHORS
Nakamura,Y.
TITLE
Structural Analysis of Arabidopsis thaliana Chromosome 5. VI
JOURNAL
Unpublished (1998)
AUTHORS
2 (bases 1 to 86064)
Nakamura,Y.
TITLE
Direct Submission
SUBMITTED (06-MAY-1998) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:++81-438-52-3935,
Fax:++81-438-52-3934)
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					Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
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					Yu,G., Theologis,A. and Ecker,J.
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
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				AUTHORS	Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R.,
					Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
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					Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
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AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,
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TITLE
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JOURNAL
Unpublished (1997)

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complete sequence.
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Nakamura.Y.
Structural Analysis of Arabidopsis thaliana Chromosome 5. VI
Unpublished (1998)
2 (bases 1 to 86722)
Nakamura.Y.
Direct Submission
Submitted (23-MAR-1998) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:yinakamu@kazusa.or.jp, Tel:+81-438-52-3935,
Fax:+81-438-52-3934)

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QY	1303	ccgaagatttgcTgtgtatccTtatcTtatcTatgTccaatgtgaagtgttgcTgtctcaag	1362
Db	71906	AAGGAGAAATGCTTGATATCCGTATCCCAAAAGGAAGCGTAGCTGATCCGTAGAG	71847
QY	1363	agaagccacccgtaac-----	1378
Db	71846	GTTTTCAATTAAACACATTTCTGTGTTTGTATTCTTTCGATATATPAACGGGAAAGTTC	71787
QY	1378	-----aaTccTgcgttattgTccaaagc	1401
Db	71786	TTATATAGTTATACATGTTTTCAGCAATATTATGAGAAAGACCGTCTCTAGATTGGAAATCGGA	71727
QY	1402	ggaagaaatccgcgttagcttagcttagctgaagttgtcttaccatcatgatactgcgac	1461
Db	71726	GGATTAACGATTGACACTCGGGGCGAGCGAGGACTTGTTAACTTTCACAGACCAATGCAATC	71667
QY	1462	cgaaTcatcatccTgacTgaaTgaagacgacaaacatccTcttgaTcgaagaaTtcgaag	1521
Db	71666	CAAAAGATTATTCACAGAGAGCGTAAAGCTGCAAATATTCCTACTTGATGAGAGCTTTGAG	71607
QY	1522	cgattgttgagaaTtcoggttggTgcaagctatgagactataaagacatccagTgacaa	1581
Db	71606	CAATAGTGTGGCGATTGTTGGCTAGCGCAAACTTTTGTAGACCAAGAGAGATTTCACATGCTACTA	71547
QY	1582	cagcaTcccgTggpacatctgTgTcaatctgcTccgaatTatctctcaacgggaatctt	1641
Db	71546	CCGAGTCCCGAGGACCATTTGGACATATGGCTCCGAGTACCTTTCCACTGACAGTCTCT	71487
QY	1642	cagaTaaaccgacgttttctgTatgagaaTatgcttcttgaacTaatcagagacaa	1701
Db	71486	CAGAGAAACGATGTTTTCGATTTGCGAGTACTAATCTTGAACCTATACAAAGTGCATA	71427
QY	1702	gaacttcgacT 1713	
Db	71426	AGATGATTGATC 71415	

Search completed: June 24, 2000, 00:38:34
Job time: 47269 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 22:46:24 ; Search time 274.21 Seconds
(without alignments)
990.258 Million cell updates/sec

Title: US-09-180-798-32

Perfect score: 2089

Sequence: 1 ggattttattttattttttt.....taaaaaaaaaaaaaaaaaaaaaa 2089

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 230463 segs, 6492525 residues

Total number of hits satisfying chosen parameters: 460926

Minimum DB seq length: 0
Maximum DB seq length: 1000000Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/6_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/PCtUS_COMB.seq:*
7: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119.4	5.7	1554	4	US-08-587-680A-24
2	93.4	4.5	2749	2	US-08-265-628-1
3	92.6	4.4	2571	1	US-07-717-331F-9
4	92.6	4.4	2833	1	US-07-717-331F-1
5	92	4.4	2749	1	US-07-717-331F-4
6	81	3.9	5733	3	US-08-473-553A-1
7	80	3.8	966	1	US-08-447-185-2
8	80	3.8	2443	1	US-08-447-185-3
9	73.8	3.5	3921	4	US-08-587-680A-3
10	73.8	3.5	3921	4	US-08-587-680A-3
11	73.8	3.5	5992	3	US-08-475-891A-3
12	70.6	3.4	6256	3	US-08-475-891A-1
13	70.6	3.4	6256	4	US-08-567-375-1
14	70.6	3.4	6256	4	US-08-567-375-1
15	68	3.3	6251	1	US-08-030-096-5
16	63	3.0	7218	1	US-08-233-463-14
17	62.4	3.0	1058	1	US-08-238-163-1
18	62.4	2.9	2075	1	US-08-238-163-3
19	57.2	2.7	831	4	US-08-567-375-15
20	55.6	2.7	7218	1	US-08-233-463-14
21	51.8	2.5	2880	4	US-08-666-271-4
22	51.8	2.5	3905	4	US-08-666-271-1
23	48	2.3	1611	1	US-07-820-011A-3
24	48	2.3	1611	6	PCT-US93-00445-3
25	47.6	2.3	13473	6	PCT-US96-03916-1
26	47.6	2.3	18912	6	PCT-US96-03916-59
27	43.6	2.1	2647	6	PCT-US93-06251-77

28	43.2	2.1	4517	6	PCT-US93-06251-83	Sequence 83, Appl
29	43	2.1	3590	1	US-08-587-889-1	Sequence 1, Appl
30	43	2.1	3590	6	PCT-US96-09193-1	Sequence 1, Appl
31	42.2	2.0	3489	4	US-08-728-323A-1	Sequence 1, Appl
32	42.2	2.0	32207	3	US-08-770-379-20	Sequence 20, Appl
33	41.2	2.0	2869	1	US-08-374-834-2	Sequence 2, Appl
34	41.2	2.0	2869	2	PCT-US95-08493-1	Sequence 1, Appl
35	40.6	1.9	2208	6	PCT-US95-08493-18	Sequence 18, Appl
36	40.6	1.9	2580	6	PCT-US95-08493-20	Sequence 20, Appl
37	40.6	1.9	2604	6	US-07-928-464-1	Sequence 1, Appl
38	40.6	1.9	2890	1	PCT-US93-07347-1	Sequence 1, Appl
39	40.6	1.9	3033	1	US-08-003-311B-1	Sequence 1, Appl
40	40.6	1.9	3033	1	US-08-261-432-1	Sequence 1, Appl
41	40.6	1.9	1920	1	US-08-186-222-1	Sequence 1, Appl
42	39.8	1.9	1251	4	US-09-211-930-2	Sequence 2, Appl
43	39.8	1.9	1251	5	US-09-340-993-2	Sequence 2, Appl
44	39.8	1.9	1353	4	US-09-211-930-8	Sequence 8, Appl
45	39.8	1.9	1353	4	US-09-211-930-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-587-680A-24
Sequence 24, Application US/08587680A
Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs

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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA (partial)
US-08-587-680A-24

Query Match          5 7%; Score 119.4; DB 4; Length 1554;
Best Local Similarity 50.1%; Pred. No. 1.9e-27;
Matches 415; Conservative 0; Mismatches 396; Indels 18; Gaps 4;

QY 1096 gtttagtaacaagaacatttggcagagtggttgggaaagctcacaaggagcgt 1155
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DB 701 GCTTGAAGAAGAACACAGCTCATAGGAGAGGTGAGCAGGAGTGTATTAAGGACTA 760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1156 tggcagaacggaactctgtgtctcagaagactgaagaagcgaaactccagtgag 1215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 761 TGCCAAATGCTGATCATGTCGCGGTGAAGAAATTGGGAATTAAGCAAGGCTCATATGATA 820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1216 agtccagttccaacagaagtagagatgaatgtagcagttcatcgaacctgttga 1275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 ACGGCTATCTG---CTGAACCTTAACACATTAGGGAAGATCAGGCATAGGTAACATTGTGA 877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1276 gattacgaggttctgtatgacaccgacgagagattgtgtgtatccttaacgtgcca 1335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 878 GACTGCTGCGCTTTTGTTCACAAAGAGATCACTTGCTATGATGACTACATGCTAA 937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1336 atggaagtgtgtctcgtgtctcagaagagagccaccgtcaacaactccgcttgatgac 1395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 938 ATGGAAGGTGTAGTGGAAGTCTTCATGCGAAGAACGCGCGGCA-----CTCCAAATGGG 991
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1396 caagcgggaagaagatcgcgtagtcacagctcgaggttgtgttacctactacatgact 1455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 992 AAACCTAGGCTTAAATATAGCCATAGACGTGCAAGGCGCTTCTTATTTGACACGATTT 1051
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1456 gcatccgaagatcatcaccgttgcgttaaaagacgaacaacatccctttagacgaagaat 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1052 GCTCCCGTATGATATCATCCGCGATGTCAAGTCCAAACATATATTTGTTGAACGTGCAAC 1111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1516 tcgaagcggtgtgttgagatttcgggttgcaag---cttatgactataaagaactc 1572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1112 TTGAAGCTCATGTTGCAAGATTTTGTGATTAGCCAAATGTTCCGTAACAAATGTACTCTG 1171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1573 acgtgacaacagcagtcgcgtgacccatcgctcacatcgctccagaaatctctcaacgc 1632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1172 AGTGCAATGCTTGCATATGCAAGGATCTTATGCTTACATTTGCTCCAGATATGATACACGC 1231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1633 gaaactctcagagaacacgacgttttcgatatcgaaatcatgtcttgaactaactca 1692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1232 TGAATAATTGATGAGAAAGGATGTATAGCTTTGGAGTGTGTGTTGAGCTTATTA 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1693 caggaacaagaagcttcgatctcgctcggttagctaaagacgacgacgtcaatgttacttg 1752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1292 CAGGACGGAAGGCCGATGGAATTTTGGAGAAAGGAAGCAATGTGTCAAAATGGGCGA 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1753 actggtggaagagttgttgaagagaagaagcagaagatgtagtgaaccagatcttc 1812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1352 AAACGGAGACAAAATGAGCAAAAGAGGGGTGTGAAAATCTTGG-----ATGAGAGGC 1405
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QY 1813 aaacaactacagagagagaactggaacaacagtatatacaagtgtgtatgacagc 1872
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DB 1406 TAAAAAATGTTGCAATTTGTAAAGCTATGCAAGTATTTTTTGTGCAATGCTTTGTGTTG 1465
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QY 1873 aagatcaccaatggaagaccaaagatgtctgaagtgtgaagaatgct 1921
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1466 AAGAGTACAGCATTTGAGAGGCTTCAATGAGGGAAGTAGTCCAATGCT 1514
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RESULT 2
US-08-265-628-1
; Sequence 1, Application US/08265628
; Patent No. 5821094
; GENERAL INFORMATION:
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;
; APPLICANT: Rothstein, Steven J.
;
; APPLICANT: Goring, Daphne
; TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
; TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison St. Suite 3400
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,628
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,945
; FILING DATE:
; APPLICATION NUMBER: US 07/847,564
; FILING DATE: 03-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien Ph.D., Donald J.
; REGISTRATION NUMBER: 32,167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-707-8889
; TELEFAX: 312-707-9155
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2749 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
; STRAIN: olifera
; INDIVIDUAL ISOLATE: W1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: S-locus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2574
; PUBLICATION INFORMATION:
; AUTHORS: GORING, DAPHNE
; AUTHORS: ROTHSTEIN, STEVEN J.
; TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
; TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A
; TITLE: FUNCTIONAL SERINE/THREONINE KINASE
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
US-08-265-628-1

Query Match          4.5%; Score 93.4; DB 2; Length 2749;
Best Local Similarity 48.9%; Pred. No. 4.4e-19;
Matches 411; Conservative 0; Mismatches 406; Indels 24; Gaps 5;

QY 1110 aacatttggcagaggtgtgttgggaaagtcatacgaaggacgttggcagaagcgaact 1169
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DB 1597 AACAACTCGACAAAGGTGTTTCGTTATTTTACAAAGGTAGATTAATTGATGCGCA 1656
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1170 ctgtgtcgtcagaagactgaaggaagcgaaactccagtgagagactccagttcaa 1229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1657 GAAATTCGCTAATAAAGGTATCAAAAACGTGCGTTCAAGGAGCTG---GTGAGTTTAG 1713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1230 acagaagtagagatgaatgaatgtagcagttcatcgaacctgttgagattacagagtttc 1289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 1714 AATGAGGTGATGATTCGCGAGGCTTCAGCATATATAACCTTGTCCGAAATTTGGCTGT 1773
QY 1290 tgtatgaacccagccagagatgtctgtgtatccttacaatgccaatggaagtgtct 1349
Db 1774 TGCATTGAGGCGACACGAGAAAGATGATGATATTTAGAAATTTAGAGCCCTCGAT 1833
QY 1350 tcgtgtcagagagagagccagccacacccctccgcttgattggccaaacgggaagaga 1409
Db 1834 TCTTATCTCTTCGGAAATTAACG---AAGCTTACGTTAAATTTGGAAGACAGATTCAC 1890
QY 1410 atcgcgtagagctcagctcagaggttcttactacatgatactcgcagctcgaagatc 1469
Db 1891 ATTACCAATGATGTTGCTCGAGAGCTTTATATCTTCATCAAGACTCAGCGTTTGGATA 1950
QY 1470 attcaecgtgaagtaagaacgaacacatccctcttagcgaagaattcgaaagcgtgtt 1529
Db 1951 ATCCACAGAGATATGAATAAGTAACTATTGCTTGATTAATAATATGACACCAAGATC 2010
QY 1530 ggaagattcgaggttggcaagcttatgagctataaagacactcag---tgacaacaga 1586
Db 2011 TCGGATTTTGGGATGCGCCAGATCTTTGCCAAGGACGAGACTGAACTTAACAAAGGAAG 2070
QY 1587 gtccgtgacacatcggtcacatcgctccaagaatactctcaacggaaatctcgaag 1646
Db 2071 GTGCTCGGAACCTTACGGCTACATGCTCCGAGATAGCAAAATGGATGGGCTATTCTCGGA 2130
QY 1647 aaaaacgaagcttctcgatacaggaatcatgctctagaactaatcaagacaagaagct 1706
Db 2131 AATTCAGATGATTTTCAGTTTGGAGTCATTTGCTTGAATTTGTTAGTGAAGAAAGAAC 2190
QY 1707 ttgcagctcgctcgctgagctaacgagcagcgtcatgcttactctgacagg-gtgaagag 1765
Db 2191 AGAGGATTTTACAACTTGAAACGCAACAAACAAATCTTAACTATGATAGGATCGTGG 2250
QY 1766 atgtgtgaaggaagaagactagagatgttagtgaatccagactctca----- 1814
Db 2251 ACGGAGGGAAGAGCCCTAGAAATTTGTTGATCCAGTCATGATTCATTTGATCATTTA 2310
QY 1814 --aacaactaagagagagagaacttggaacaagtatacaagtgagcgttctgatacgag 1871
Db 2311 CCAGCAGACCTTTCAACCAAAAGAAAGTTCTAAATATGCATCAAAATTTGCTCTT 2370
QY 1872 caagagtaaccaatggaagaagacaaagatgtctgaagttgtaagagtgatgaagaagt 1931
Db 2371 CAGGAACGTGCAGAGCATAGACCAAGATGTGCTCGGTGTTGGATGCTTGAAGTGA 2430
QY 1932 g 1932
Db 2431 G 2431

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; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/717,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-07-717-331F-9

Query Match 4.4%; Score 92.6; DB 1; Length 2571;
Best Local Similarity 49.6%; Pred. No. 7,se-19;
Matches 323; Conservative 0; Mismatches 319; Indels 9; Gaps 3;

QY 1110 aacatttggcgagaggtgttgggaagctcacaagagcgttggcagaggaact 1169
Db 1594 AACCAATCGGACCAAGGCGTGTGTTGTTTACCAAGGGAAGATTCCTTGACGGGAAA 1653
QY 1170 ctgtgtgtcgaagaagctgaagaagcgaactccaggtgagagctccagttcaca 1229
Db 1654 GAATTTGCAATTAAGGCTTATCAAGACGTCAGTTCAGAGGACTGATG---AGTTTATG 1710
QY 1230 acaagaagaagatgataagtaatgagcagttcatcgaaacctgtgagattacagaagttc 1289
Db 1711 AATGAGTGACACATTAATGCGAGGCTTCAGCATATAAACCCTTGTTCAGATTTCTGGCTGT 1770
QY 1290 tgtatgaacccagccagagatgtctgtgtatccttacaatgccaatggaagtgtct 1349
Db 1771 TGCATTGAGGAGATGAAAGATGATGATATGATATGATTTGGAAATTTAAAGCCTTGAT 1830
QY 1350 tcgtgtccagagagagccacccgtcacacactccgcttgatttggccaacgaggaagaga 1409
Db 1831 TCTTATCTCTTTG---GTAAACCCGAAGCTTAAAGCTTAATTTGAAATGAGATTCGAC 1887
QY 1410 atcgcgtaggctcagctcagaggttcttactacatgatactcagctcgaagatc 1469
Db 1888 ATTACCAATGCTGTTGCTCGAGGCTTTTATATCTTCATCAAGACTCACGGTTAGGATA 1947
QY 1470 attcaecgtgaagtaagaagcgaacactcctcttaagaagaatccgaagcgttgtt 1529
Db 1948 ATCCACAGAGATTTGAAGTAAGTAACTTTTGGCTTGCAAAAAATATATGATCCCAAGATC 2007
QY 1530 ggaagattcgaggttggcaagcttatgagctataaagacactcag---tgacaacaga 1586
Db 2008 TCGGATTTTGGGATGCGCCAGATATTTGAAGGACGAAGCAAGCTTAACCAATTAAG 2067
QY 1587 gtccgtgacacatcggtcacatcgctccaagaatactctcaacggaaatctcgaag 1646
Db 2068 GTGCTCGGAACATAGCGCTCATATGCCCCGGAATATGCAAGCAATGTATGGAATATTCGGA 2127
QY 1647 aaaaacgaagcttctcgatacaggaatcatgctctagaactaatcaagacaagaagcgt 1706
Db 2128 AATTCAGATGTTTTCAGTTTGGAGTCTATGATTTCTTAATAATTTGTTAGTGAAGAAAGAAC 2187
QY 1707 ttgcagctcgctcgctgagctaacgagcagcgtcatgattactgagctagg 1757
Db 2188 AGAGATTTCTACAACTTGAGACTACGAAACGATCTCTTAAGCTATGATAG 2238

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RESULT 4
US-07-717-331F-1
; Sequence 1, Application US/07717331F

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; Patent No. 5484905
; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/717,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-07-717-331F-1

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Query Match 4.4%; Score 92.6; DB 1; Length 2833;

Best Local Similarity 49.6%; Pred. No. 8e-19;

Matches 323; Conservative 0; Mismatches 319; Indels 9; Gaps 3;

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QY 1170 ctgtgtgtcaagagactgaagaaagcgaactccaggtgagagctcagttcaa 1229
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DB 1654 GAAATTGCAGTAAAGGCTATCAAAAGACGTCAAGGAGGAGCTGATG--AGTTTATG 1710
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QY 1230 acagaagtagagatgataagtatgagcagttcaatcgaacctgttgaattcagagtttc 1289
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DB 1711 AATGAGGTGACACTAATTGCGAGGGCTTATGATATAAACTTGTTCAAGTCTTGCGCTGT 1770
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1280 tgtatgacacgacgacgagatgtgtgtatctcttaacgtccaaatggaagtgttgc 1349
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1771 TGCATTGAAGCAGATGAGTAAGATGTTGATATATGAGTATTGGAAAAATTTAAAGCTTGTAT 1830
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QY 1350 tctgtctcagagagagccaccgtcacacacctccgcttgaattggcacaacgcygaagaga 1409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1831 TCTTATCTCTTTG--GTAATAACCCGAAAGGTCTAAGCTAAATTGGAATGAGAGATTGAC 1887
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1410 atcgcgtagagctcagctcagagtttcttaactacatgacatcgatcgatcgaagatc 1469
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1888 ATTACCAATGGTGTGCTCGAGGGCTTTTATATCTTCAATCAAGACTCAGGGTTTATAGGATA 1947
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QY 1470 attccgctgaagtaaaagcgaacacatcctcttagcgcgaagattcgaagcggtgttct 1529
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QY 1530 ggaagtttcgggttgccaacacttaagactataaagacactcag---tgacaacagca 1586
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DB 2068 GTGTCGGAACATACGGCTCATATGTCGCCGGAATACGAATGTATGGATATTCTCGGAA 2127
QY 1647 aaaccgagcttttcgatatcgaatcgtctcttaagaactaacatcacagacaagaagct 1706
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DB 2128 AATTCAGATTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTAGTGGAAAGAAAGAC 2187
QY 1707 ttcgattcgtcgcgtcagtagtaagcagacgaatcgtatcttactgactg 1757
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DB 2188 AGAGGATTTCAACAATTGACACTGCAAAACGATCTCCTAAGCTATGTATAGG 2238

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RESULT 5
US-07-717-331F-4
; Sequence 4, Application US/07717331F
; Patent No. 5484905

GENERAL INFORMATION:

APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua

APPLICANT: Stein

TITLE OF INVENTION: A Receptor Protein Kinase Gene

TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates

STREET: 25 Skytop Drive

CITY: Trumbull

STATE: Connecticut

COUNTRY: USA

ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/717,331F

FILING DATE: June 19th 1991

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 2749 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-07-717-331F-4

Query Match 4.4%; Score 92; DB 1; Length 2749;

Best Local Similarity 50.7%; Pred. No. 1.2e-18;

Matches 302; Conservative 0; Mismatches 285; Indels 9; Gaps 3;

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QY 1110 aacatttggcagaggtgttggaagtctacaaggagccttggcagcaggaact 1169
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DB 1612 AACCAAGTCCGAAAGGtgggttggatgtttacaaagggaagttaCTTGACGGGCAA 1671
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QY 1170 ctgtgtgtcaagagactgaagaaagcgaactccaggttgaagagctcagttcaa 1229
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DB 1672 GAATTCAGATGAAGAAGTATGGAATGTCAAGCTCAAGGTACGATG--AGTTCATG 1728
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QY 1230 acagaagtagagatgataagtatgagcagttcaatcgaacctgttgaattcagagtttc 1289
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DB 1729 AAGCAAGTTAGCTAATGCAAAAGCTTACGACCAATATATCTTGTCCGACTTCTTGCGCTGT 1788

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QY	1290	tgatgaccgagccagagaaatgctgtgtatcccttaacatgccaatggaggttgc	1349
	1789	TGCTTTATATAGGGCCGAGAGACTTTAAATTACAGACTTTTGAGAACTTAAGCCTCAT	1848
QY	1350	tcgtgtctcagagagagccaccgtcacacactccgcttgatctggccaacgcggaagaga	1409
Db	1849	TCCTATCTCTTGA---TGAAACCAAGACTGTATGTTAAATTGGCAATAGATTTGAT	1905
QY	1410	atcgcgtaagctcgaagctcgaagttgtcttaactacatgatactcgaatcgatccgaatc	1469
Db	1906	ATATATCATATGGTATATGGCCGAGGGCTTCCTATCTTACCAAGATTCACGGTTTGAATTC	1965
QY	1470	attaccgttacglaaaagagcaaacatccctcttagagagaatlcgaagcggttgt	1529
Db	1966	ATCCACAGGGGTTTGAAGCAGCAATGCTTGCTTGATTAAGAATATGATCTCCAAAAATT	2025
QY	1530	ggagatttcgggttgccaaagctctatgacataaagaaccca---cgtgcaacagca	1586
Db	2026	TCAACCTTTGGAAATGCGTATAGATCTTTGGACGGGATGAAACGGAAAGCTGACACAGGAAG	2085
QY	1587	gtccgtggaacacgcgttcacatcgctccaagaatatcttcaaccggaanaalcitcagag	1646
Db	2086	GTGCTCGGAACCTATATGCGTCATGCTCTCCAGAAATATGCATGAACGGGCAATTCATCATG	2145
QY	1647	aaacccagcgttttcgatacgaatcaatcagtccttctgaactatatacagagcaaaag	1702
Db	2146	AAGTCATATGTTCACTTTTGGGGCTCTGCTCTTGAATATATAGTGGCAAGG	2201

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1      RESULT      6
2      US-08-473-553A-1
3      : Sequence 1, Application US/08473553A
4      : Patent No. 5859338
5      : GENERAL INFORMATION:
6      : APPLICANT: Meyerowitz, Elliot M.
7      : APPLICANT: Clark, Steven E.
8      : APPLICANT: Williams, Robert W.
9      : TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
10     : TITLE OF INVENTION: Transformed Plants, and Proteins
11     : NUMBER OF SEQUENCES: 11
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
14     : STREET: Four Embarcadero Center, Suite 3400
15     : CITY: San Francisco
16     : STATE: California
17     : COUNTRY: United States
18     : ZIP: 94111-4187
19     :
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Floppy disk
22     : COMPUTER: IBM PC compatible
23     : OPERATING SYSTEM: PC-DOS/MS-DOS
24     : SOFTWARE: Patentin Release #1.0, Version #1.30
25     : CURRENT APPLICATION DATA:
26     : APPLICATION NUMBER: US/08/473,553A
27     : FILING DATE: 06-JUN-1995
28     : CLASSIFICATION: 800
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: Silva, Robin M.
31     : REGISTRATION NUMBER: 38,304
32     : REFERENCE/DOCKET NUMBER: A-60886/RT/RTMS
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: (415) 781-1989
35     : TELEFAX: (415) 398-3249
36     : TELEX: 910 277299
37     : INFORMATION FOR SEQ ID NO: 1:
38     : SEQUENCE CHARACTERISTICS:
39     : LENGTH: 5733 base pairs
40     : TYPE: nucleic acid
41     : STRANDEDNESS: unknown
42     : TOPOLOGY: unknown
43     : MOLECULE TYPE: DNA (genomic)
44     : FEATURE:
45     : NAME/KEY: CDS
46     :
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; NAME/KEY: CDS
; LOCATION: 5117...5467
;
US-08-473-553A-1

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Query Match	3.9%	Score 81;	DB 3;	Length 5733;
Best Local Similarity	49.9%;	Pred. No. 6e-15;		
Matches 235;	Conservative	0;	Mismatches 230;	Indels 6;
			Gaps	1;

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QY	1152	cgttggagagacggaactctgtgtgtcgtcaagagactgaagaagaggaactccagtc	1211
Db	4576	TCAATGCCAAACAACGTAAGACGTGGCATTAAACGACTGGTTGGCCGTGGACCGGGAGG	4635
QY	1212	gagagctccagttccaagaagaagtatgatatgcatatgacgtcatcgaacctg	1271
Db	4636	AGCGATCATGGATTTCACGGCGGAGGAGATTCAACTTTGGGGGAATCCGCCACCGTCACTA	4695
QY	1272	ttgagattacagagttctctgatatacaacgacagagattgcttgatccttaacg	1331
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Db	4756	CGTATGSAAGCCTTTGGAGAGCTTTTCATGG-----ATCTAAAGGTGGTCACTCTTCA	4809
QY	1332	tggcacacgcggaagagaatccgcgtcgtacgtcagctcgaagtttgccttaactacatgat	1451
Db	4810	TGGGAGACGACACATATAGAGTAGCCGTTGGAAAGCTGCAAAAGGGCTTGCTATCTTCCACAT	4868
QY	1452	cactgcgcgtccgaagatcaatcaacgtgacgtgaacaaagcagcaaacatcctcttaagcaa	1511
Db	4870	GATTGTTCCACCATTTGATCTTGCATAGAGATGTTAACTCAATTAACATCTTTTGGACACT	4928
QY	1512	gaattcgaacgaggttttttggaatttcggtttggcgaagcttaagacct	1562
Db	4930	GATTTTGAAGCCCATGTGTCTGATTTTGGGCTTGTCTAGTCTTATTCAT	4980

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1      RESULT 7
2      US-08-447-185-2
3      ; Sequence 2, Application US/08447185
4      ; Patent No. 564859
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Tanksley, Steven D.
8      ; APPLICANT: Martin, Gregory B.
9      ; TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
10     ; TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH
11     ; NUMBER OF SEQUENCES: 5
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Michael L. Goldman
14     ; STREET: Clinton Square, P.O. Box 1051
15     ; CITY: Rochester
16     ; STATE: New York
17     ;
18     ; COUNTRY: U.S.A.
19     ;
20     ; ZIP: 14603
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: Patentin Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/447.185
29     ; FILING DATE:
30     ; CLASSIFICATION: 800
31     ;
32     ; PRIOR APPLICATION DATA:
33     ; APPLICATION NUMBER: US/08/111.078
34     ; FILING DATE:
35     ;

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1      RESULT 7
2      US-08-447-185-2
3      ; Sequence 2, Application US/08447185
4      ; Patent No. 564859
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Tanksley, Steven D.
8      ; APPLICANT: Martin, Gregory B.
9      ; TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
10     ; TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH
11     ; NUMBER OF SEQUENCES: 5
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Michael L. Goldman
14     ; STREET: Clinton Square, P.O. Box 1051
15     ; CITY: Rochester
16     ; STATE: New York
17     ;
18     ; COUNTRY: U.S.A.
19     ;
20     ; ZIP: 14603
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: Patentin Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/447.185
29     ; FILING DATE:
30     ; CLASSIFICATION: 800
31     ;
32     ; PRIOR APPLICATION DATA:
33     ; APPLICATION NUMBER: US/08/111.078
34     ; FILING DATE:
35     ;

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RESULT 9

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US-08-567-375-3
? Sequence 3, Application US/08567375
? Patent No. 5952485
?
? GENERAL INFORMATION:
? APPLICANT: Ronald, Pamela C.
? APPLICANT: Wang, Guo-Liang
? APPLICANT: Song, Wen-Yuang
? APPLICANT: Szabo, Veronique
? TITLE OF INVENTION: Procedures and Materials for Confering
? TITLE OF INVENTION: Disease Resistance in Plants
? NUMBER OF SEQUENCES: 16
?
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3634
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/567,375
? FILING DATE: 04-DEC-1995
? CLASSIFICATION: 800
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/004,645
? FILING DATE: 29-SEP-1995
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/475,891
? FILING DATE: 07-JUN-1995
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/373,375
? FILING DATE: 17-JAN-1995
?
? ATTORNEY/AGENT INFORMATION:
? NAME: Bastian, Kevin L.
? REGISTRATION NUMBER: 34,774
? REFERENCE/DOCKET NUMBER: 023070-058930
?
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
?
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3921 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
?
? NAME/KEY: CDS
? LOCATION: join(1..2676, 3520..3918)
? OTHER INFORMATION: /product="Xa-21"
US-08-567-375-3

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Dd	1198	ATTGGCTCACAACATCTCTVMTCTCTGCACMACMAAAATTTAGAGGGGTCTCTCATCATCTCG	1257
Oy	603	cttgggaagcttccaagcgtagattcttcgcgctaacaacaaacyctaccctggtcca	662
Dd	1258	TTGGCCAGGCTTAANAACCTTAGGCGATTCTACTGCGCTACGAAAACACTTGGACGGTTTG	1317
Oy	663	attcctaigtacacgaccaatatcatccctccaagtgltagatctalcaaatcaataga	722
Dd	1318	ATMCCGTTGGCCATAGAAATACTTACTGAACTTAATATCTTACTGCTGGCACCAACANA	1377
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US-08-587-680A-3
: Sequence 3, Application US/08587680A
: Patent No. 5977434
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: GENERAL INFORMATION:
:
: APPLICANT: Ronald, Pamela C.
: APPLICANT: Wang, Guo-Liang
: APPLICANT: Song, Wen-Yuang
: APPLICANT: Szabo, Veronique
: TITLE OF INVENTION: Procedures and Materials for Confering
: TITLE OF INVENTION: Disease Resistance in Plants
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
: ADDRESS: Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/587,680A
: FILING DATE: 17-JAN-1996
: CLASSIFICATION: 800
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,375
: FILING DATE: 17-JAN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/475,891
: FILING DATE: 07-JUN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/004,645
: FILING DATE: 29-SEP-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/567,375
: FILING DATE: 04-DEC-1995
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 023070-058940US
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEQ ID NO: 3:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3921 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single

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REFERENCE/DOCKET NUMBER: 02370-0589100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
US-08-475-891A-1
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Query Match 3.4%; Score 70.6; DB 3; Length 6256;
Best Local Similarity 53.9%; Pred. No. 1.2e-11;
Matches 145; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
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DB 2866 ATTGGCTTACACACTCTCTATCTCTGCAACACAAATTTGAGAGGTCACCTTCATCATG 2925
QY 603 ttgggaagcttcaaaagctgagattctccggtcttaacaacaagctcactgggtca 662
DB 2926 TTGGGCGAGGCTTAGAAACTTAGGCAATTCATGTCGCTACGAAACAACTTGACCGGTTTG 2985
QY 663 attcctagtcacagcaacataattactacccttcaagtgtagatctatacaataacaga 722
DB 2986 ATCCCATTTGGCCATAGGAATCTTACTGACACTTAATATCTTACTGCTGGGACCAACAA 3045
QY 723 ctctctggttcagttcctgacaatgctc 751
DB 3046 TTCAGTGGTTGATACCATACACACTCTC 3074
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RESULT 13
US-08-567-375-1
; Sequence 1, Application US/08567375
; Patent No. 5952485
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Szabo, Veronique
; TITLE OF INVENTION: Procedures and Materials for Confering
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,375
; FILING DATE: 04-DEC-1995
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice
US-08-567-375-1
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Query Match 3.4%; Score 70.6; DB 4; Length 6256;
Best Local Similarity 53.9%; Pred. No. 1.2e-11;
Matches 145; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
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QY 543 acaactagtagttagttagcttacttaacagcttcccggtccttccttcggaatca 602
DB 2866 ATTGGCTTACACACTCTCTATCTCTGCAACACAAATTTGAGAGGTCACCTTCATCATG 2925
QY 603 ttgggaagcttcaaaagctgagattctccggtcttaacaacaagctcactgggtca 662
DB 2926 TTGGGCGAGGCTTAGAAACTTAGGCAATTCATGTCGCTACGAAACAACTTGACCGGTTTG 2985
QY 663 attcctagtcacagcaacataattactacccttcaagtgtagatctatacaataacaga 722
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QY 723 ctctctggttcagttcctgacaatgctc 751
DB 3046 TTCAGTGGTTGATACCATACACACTCTC 3074
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US-08-587-680A-1
; Sequence 1, Application US/08587680A
; Patent No. 5977434
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Szabo, Veronique
; TITLE OF INVENTION: Procedures and Materials for Confering
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
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STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
OTHER INFORMATION: sativa)"
US-08-587-680A-1
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Query Match 3.4%; Score 70.6; DB 4; Length 6256;
Best Local Similarity 53.9%; Pred. No. 1.2e-11;
Matches 145; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 483 tatttgagcttaccagtaacacataactgcccgaattcctagtaatttgaaatctg 542
DB 2806 TTCTTCGACCTTGATTGAATAATGATCAGAGAGCATTTCCAAAGATATTGGCAATCTT 2865
QY 543 acaactatgagagtttgatcttacttaaacagcttcttcgcttacttccggaatca 602
DB 2866 ATTGGCTTACAAACATCTCTATCTCTGCAACAAACATTTCAGAGGGTCACTTCATCTCG 2925
QY 603 ttgggaagcttcaaaagctgagattctccggtttaacaacacagcttcaactgggtca 662
DB 2926 TTGGGACAGCTTAGAAATTTAGGCACTTGTAGTCCGCTACGAAACAACTTAGAGGGTTG 2985
QY 663 attcctatgtaactgacacataatactacccttcaagtggttagatctataaatacaga 722
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QY 723 ctctctggttcaagttcctcgacaatggctc 751
DB 3046 TTCAAGTGGTGGATACCATACACTCTC 3074
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RESULT 15
US-08-030-096-5/c
Sequence 5, Application US/08030096
Patent No. 5426041
GENERAL INFORMATION:
APPLICANT: Fabijanski, Steven F.
APPLICANT: Arnison, Paul G.
TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
TITLE OF INVENTION: SEED PRODUCTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,096
FILING DATE: 22-MAR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/556,917
FILING DATE: 20-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA91/00255
FILING DATE: 22-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/164/PLHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3641 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(854..1105, 1266..2375, 2463..2779)
US-08-030-096-5
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Query Match 3.3%; Score 68; DB 1; Length 3641;
Best Local Similarity 51.5%; Pred. No. 5.4e-11;
Matches 235; Conservative 0; Mismatches 210; Indels 11; Gaps 3;

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DB 3639 TAGACCAACACTTTCACAGCACCGCTCTCGACTTGTGATGCAAGGCTGTGACGCTC 3580
QY 1564 aagacacatcagctgaacaagca--gtccgtgacacatcggttcacatcgctcagaata 1621
DB 3579 TGGACACGCAATTGAGCGGACACACGCTCGCGGAACTCCCGGTTACGTTCCGCGAGACTA 3520
QY 1622 tctctaacgcggaanaattcttcagagagaacacgagcttttcgatacggaatcaagcttct 1681
DB 3519 TTACGAGATTTCAGGTGACGACACCAAMAGAGATGTGATACCTTACGCGGTTATACCTTCT 3460
QY 1682 agaactacacagacgaagaagcttttcgattctgctcgctagcttaacgcgagacgt 1741
DB 3459 GGAAGTTCTCTCGGGGAACAAACCATGATGATCAGAGAGATTGGTGAAGACAAACATCT 3400
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QY 121 atttcggaagtttaggggtttcttcggaatcgaagatcaaatcaaatccgaattcgaattac 180
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 Db 121 ATTTCGGAAGTTAGGGGTTTCTCGATCTGAAAGATCAAAATCAAAATTCGAAATTTAC 180
 QY 181 catgtgtttgaaatagagtcgagttatgtgtgtatcatcttcaactgaattac 240
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 Db 181 CATGTGTTTGAATGGAATGAGTCGAGTTATGTGTATTATCTTCACTTGATCTTAC 240
 QY 241 ttccgaatcaatcactgtgtgtctctcgtctaatctggaaagtgtatgtcttgaactc 300
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 Db 241 TTCCGAATCATTCACGTGTGCTTCTCTGTAATTTGGAAGTGATGCTTTTGATCTT 300
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 Db 301 TGAGGTTACTGTAGTTATCCAAACAAATGCTTTCAGAGCTGGATCTTACGCTTATGTA 360
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 Db 361 ATCCCTTGACATGCTTCATGTCACACTTGCACAAACGAGAAAGTGCATATGATTTGATT 420
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 Db 421 TGGGGAATGCAGAGTTATCTGGCCATTTAGTTCAGAGCTTGTGTCTCAAGAATTTGC 480
 QY 481 agtatcttgagctttacagtaacaacaataactgtgcccagattccctagtaaatcttggaaatc 540
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 Db 481 AGTATTTGGAGCTTTACGATTAACAAATTAATCTGGCCGATTCCTAGTATCTTGGAAATC 540
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 Db 541 TGACAAATCTAGTGAAGTTGATCTTTACTTAAACAGCTTCCGGTCCCTATTCGGGAAT 600
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 Db 961 CAATGACCTTGTGCTGTGTGCGAGAGAAGGCCACTGATATATTCTTCATGTCCTGTG 1020
 QY 1021 ccgaagaagaatccagaagttcaatctgtggacaagctccaagaagtttcttgcgggaagctac 1080
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 Db 1081 AAGTGCGAGTATGTGCTTTACTTAACAAGACATTTTGGCGAGAGTGGGTTTGGGAAG 1140
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 Db 1141 TCTACAAGGAGCAGCTTGGGACAGACGAACTCTGTGTCAAGAGACTGAAGAAAGAC 1200
 QY 1201 gaactccagtgtagagagctccagttccaacaagaagtgtagatgaatagttatgagcttc 1260

Db 1201 GAACTCCAGGTGAGAGCTCCAGTTTCAAAACGAAGTGAAGATGATAGTATGGCAGTTTC 1260
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 Db 1381 CTCCGCTTATGTGGCCAAAGCGGAAAGAAATCGCGCTAGAGCTCAGCTCGAGGTTGTCTT 1440
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 Db 1441 ACCTATGATGATCACTGCTCGATCCGAAGATCATTCACCGTGAATAAACGACCAACATCC 1500
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 Db 1621 ATCTTCAACCCGGAATAATCTTCAAGAAAAACGACGCTTTTCGATACGGAATCAATGCTTC 1680
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 Db 1801 ATCCAGATCTTCAAAACAAACTACGAGGAGAGAGAACTGGAACAAATGATCAACATGGCGCT 1860
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 Db 1861 TGCTATGCAAGCAAGGATCCCAATGAAAGAACCAAGATGCTGAAGTTGTAAAGGATGC 1920
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 Db 1981 AAGAGATGATTTGAGTCTCAATCCTTAACCTGATGTGATTTCTGTGATTTCTACTCAAT 2040
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 Db 2041 TGCAAGCGCTTGAATTAATCTGTCTCAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAG 2089

RESULT 2

V06571
 ID V06571 standard; cDNA; 1814 BP.
 AC V06571;
 DT 03-AUG-1998 (first entry)
 DE Daucus carota SERK gene.
 KW receptor kinase; apomixis; apomictic; seeds; production; embryos;
 OS Daucus carota.
 FH key
 FT CDS Location/Qualifiers
 FT 94..1755
 FT /tag= a
 FT /product= SERK protein

V06585
ID V06585 standard; DNA: 4081 BP.
AC V06585;
DT 03-AUG-1998 (first entry)
DE Arabidopsis thaliana SERK gene.
KW receptor kinase: apomixis; apomictic; seeds; production; embryos;
KM plant breeding; ds.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 3696..6620
FT FT /tag= a
FT FT /note= "contains introns"
FT FT 3731..3802
FT Intron /tag= b
FT FT /number= 1
FT FT 3851..3979
FT Intron /tag= c
FT FT /number= 2
FT FT 4124..4211
FT Intron /tag= d
FT FT /number= 3
FT FT 4284..4357
FT Intron /tag= e
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PD WO9743427-A1.
PD 20-NOV-1997.
PR 13-MAY-1997; E02443.
PR 14-MAY-1996; GB-010044.
PA (NOVS) NOVARTIS AG.
PI De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;
DR WPt: 98-086529/08.
DR P-PSDB: W47017.
PT Production of apomictic seeds - useful in plant breeding
PS Claim 26; Pages 64-67; 123pp; English.
CC The sequence is that encoding SERK, a putative receptor kinase.
CC It may be used as part of a method of producing apomictic seeds
CC comprising: (a) transforming plant material with a nucleotide
CC sequence encoding a protein which in active form in a cell or
CC cell membrane renders the cell embryogenic; (b) regenerating
CC the transformed material into plants or carpel-containing
CC plant parts; and (c) expressing the sequence in the vicinity
CC of the embryo sac. The apomictic seeds and embryos thus produced
CC can be developed into plant progeny. This is useful in plant
CC breeding programs. Controllable and reproducible apomixis provides
CC many advantages in plant improvement and cultivar development in
CC the case that sexual plants are available as crosses with the
CC apomictic plant. Apomixis provides for true-breeding, seed
CC propagated hybrids and could shorten and simplify the breeding
CC process so that selfing and progeny testing to produce and/or
CC stabilise a desirable gene combination could be eliminated.
CC Apomixis allows plant breeders to develop cultivars with
CC specific stable traits for such characteristics as height,
CC seed and forage quality and maturity.
SQ Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;

Query Match 25.9%; Score 540.8; DB 1; Length 4081;
Best Local Similarity 85.3%; Pred. No. 1e-140;

	Matches	665; Conservative	0; Mismatches	2; Indels	113; Gaps	1;
QY	1018	ctgcggaagaagatccagaagttcattcgtggacagctcaagaagtttcttctggggagc			1077	
DB	3302	CAGCCGAAGAAGATCCAGAAGTTCACTCTGGACACTCAAGAGTTTCTTGGCGGAGC			3361	
QY	1078	tacaagtgccgagtgatggttttagtaacaagaacatttggcagaggttggttggga			1137	
DB	3362	TACAAATGGCGAGTGAATGGTTTATGACAAACATTTTGGCGAGAGTGGGTTGGGA			3421	
QY	1138	aagcttacaagagacgttggcagacagacactctgttgcctgtccaagaagactgaagaag			1197	
DB	3422	AAGTCTCAAGAGGACCGCTTGGCAGAGGAACTTGTTGCTCTCAAGAGACTGAAGGAAG			3481	
QY	1198	agcgaaatccaggtgagagagctcagttcaaacgagaagtagagatgataatgagcag			1257	
DB	3482	AGCGAACTCCAGGTGAGAGCTCCAGATTCCAAGAAATAGATGATGATATATATGCGAG			3541	
QY	1258	ttcatcgaaacctggttgagattagagagtttctgtatgacccgagcgagagattgcttg			1317	
DB	3542	TTTATCGAAACCTGTGACATTTACGAGTTTCTGTATGACCGAGCCGAGATTTGCTTG			3601	
QY	1318	tgatccttacaatgagcgaatggaagtgtgtctgtcgtgtctcag-----			1361	
DB	3602	TGTATCCTTACATGGCCATGGAAGTGTGCTTCGTCTCAGAGGTAAACTAAACAA			3661	
QY	1361	-----			1361	
DB	3662	TTAACATCTTGTGCTCTCTCATATTACTTTGACGTGAAGTGTTTTTCATGTTTCTT			3721	
QY	1361	-----			1384	
DB	3722	TTATGGTTCATATTGTTGTTTACACTAATGACACAGAGAGGCCCGTCAACACCTCC			3781	
QY	1385	gcttgattggcgaagcgaagaaatcgcgcgtcaggtcagctcgaaggttgcttacct			1444	
DB	3782	GCTTGATTGGCCAAACCGGAGAAATCCGCTAGACTCAGTCCGAGGTGCTTTACTT			3841	
QY	1445	acatgatactgcgatacgaagaatcattacacgtgacgtaaaagcgaacaacatcctct			1504	
DB	3842	ACATGATCACTGCGATCCGAAGATCAATCAACGTGACGTAAAGACCAACATCTCTT			3901	
QY	1505	agacgaagaattcgaagcgttcttgagaatttcggttgcgaagctatagactataa			1564	
DB	3902	AGAGGAAGATTTGGAAGCGGTTTGTGAGATTTGGGTTGGCAAGCTAATGACTATTA			3961	
QY	1565	agacactcacgtgaacaacagcagtcctgtgacacatcgtgtacacatcgtctcagaatatc			1624	
DB	3962	AGACACTCACGTGACAAACAGCACTCGTGACCAATCGGTCAATCGCCAGAAATATCT			4021	
QY	1625	ctaacccggaatacttcagaagaacacgagcttttcgatacgaatcgtctctaga			1684	
DB	4022	CTCAACCGGAATAATTCAGAGAAACCGACGTTTTCGATACGGAATATCTCTTAGA			4081	

RESULT 4
ID V06570 standard; DNA: 6695 BP.
AC V06570;
DT 03-AUG-1998 (first entry)
DE Daucus carota SERK gene.
KW receptor kinase: apomixis; apomictic; seeds; production; embryos;
KM plant breeding; ds.
OS Daucus carota.
FH Key Location/Qualifiers
FT CDS 3696..6620
FT FT /tag= a
FT FT /note= "contains introns"
FT FT 3731..3802
FT Intron /tag= b
FT FT /number= 1
FT FT 3851..3979
FT Intron /tag= c

Query Match	10.1%	Score 211.8;	DB 1;	Length 788;
Best Local Similarity	63.0%;	Pred. No. 2e-49;		
Matches 327;	Conservative 0;	Mismatches 192;	Indels 0;	Gaps 0;
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DB 86 GCAAACTCCGAGAGAGATGCTTTACGCTCTTCGCCGAGTTTAAACAGATCCGACCAT	145			
QY 330 gcttcgagagcttggatctcctacgcctagtgaaaccccttgacacatggttccatgttcacttgc	389			
DB 146 GTTTCACAGAGCTGGGATCCAACTCTGTGTATTCCTTGACCTGGTTCATGTCACTGT	205			
QY 390 aacaacagagaacagtgctcaagaagtgtatttggggaaatgcagagttatctgccaattta	449			
DB 206 AACCAAGACAAACGGCGCTCACTGCTGTGGATTTGGGGAAATTCAAACCTCTGTGACATCTT	265			
QY 450 gtccagagagcttggctgtgtctcaagaatttgcagatttggagctttacagttacagata	509			
DB 266 GCGCTGAGCTTGGGAGAGCTTTAAACATTTACAGTATCTGAGCTCTTACAAAACAAACATC	325			
QY 510 actgcccagcttccctcctagtaatcttggaaactctgacaaacttgaagtgttgatcttac	569			
DB 326 CAAGGAACATATACCTCCGAACTCGAAATCTGAAGAATCTCATCAGCTTGATCTGTAC	385			
QY 570 ttaaacagcttcccggtctcattcccggaatatttgggaaagcttcaagcttgattt	629			
DB 386 AACCAACATCTTACAGGGATGTAGTCTCCACTCTTTGGGAAATTTGAAGTCTGTGCTTT	445			
QY 630 ctccgagcttaacaacaacagctcactggtgctcaattcctatctacactgacccaattact	689			
DB 446 TTACGGCTTAAATGACAACCGGATTGACGGGGCAATCCCTAGAGCATCCTGCCAATCCA	505			
QY 690 acccttcaagtgttgatctatccaataacagactctcgtgttcagttcctgacaatgac	749			
DB 506 AACCTTAAAGTTGTGATGCTCTCAAGCATGATTTGTGTGGAAACAATCCAAACAACGGA	565			
QY 750 tccctcactcttccaccacatcagtttggtaataac	788			
DB 566 CCTTTGCTCACATTCCTTTACAGAACTTTGAGAACAC	604			
RESULT 6				
ID V06590	standard; cDNA to mRNA; 1063 BP.			
AC V06590.				
DT 03-AUG-1998	(first entry)			
DE Arabidopsis thaliana SERK LRR homologous EST clone.				
KW receptor kinase; apomixis; apomictic; seeds; production; embryos;				
KN plant breeding; leucine-rich repeat; ss.				
OS Arabidopsis thaliana.				
PFH key	location/Qualifiers			
FT CDS	106..762			
FT FT	/*tag= "a			
FT FT	/note= "shows high homology to SERK"			
PN WO9743427-A1.				
PD 20-NOV-1997.				
PF 13-MAY-1997: E02443.				
PR 14-MAY-1996; GB-010044.				
PA (NOVS) NOVARTIS AG.				
PI De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;				
DR WPI: 98-086529/08.				
DR P-PSDB: 0467022.				
PT Production of apomictic seeds - useful in plant breeding				
PS Claim 28; Pages 86-88; 123pp; English.				
CC The sequence is that of an EST clone showing high homology to				
CC SERK LRR (leucine-rich repeat) sequences.				
CC Sequence 1063 BP; 313 A; 242 C; 206 G; 302 T;				

QY	270	gctcaatttgaaagtgatgactgcttgcatactcttgagggctgactctgattgattgccaaacat	329
Db	184	GCMAAATCCGGAAGGAGATGCTTTACCGCTCTTCCCGGAGTTAAACAGATTCGGACAT	243
OY	330	gtctcgagagcttgatgactcctacgctagtgaaatcccttcacatggtcttcacgtcctgc	389
Db	244	GTTCCTCCAGAGCTGGGATCCAACTTTGTTAATCTTGTACTGGTTCCATGATCACTGT	303
OY	390	aacacagagaaacagtgatcataagattgatttgggaaatgcagagttatctggccattta	449
Db	304	AMCAAGAACAAACCGGTCACCTGCTGGATTTGGGGAATTCAAACCTCTGTGACATCTT	363
OY	450	gttccagagcttggtgtgtctcaagaatttgcaatattggagcttcaatgaacaacta	509
Db	364	GGCGCTGAGCTTGGGAAGCTTGAACTTTACAGTATCTAGACCTCTTAAACAAACATTC	423
OY	510	actgcccagattccctcagtaactcttgaaatctgcagaaactagtgagcttgatcttac	569
Db	424	CAGGAACTATACCTTCCGAACTTGGAAATCTGAAAGAAATCATAGCTTGATTTGAC	483
OY	570	ttaaacagctctccgctctcattctccggaatcattgggaaagcttcaaaagctgagatt	629
Db	484	AMCAACATCTTACAGGGGATTAATTCCCACTTGTGGGAAATTCAGTCTGTGCTTT	543
OY	630	ctcggcttaacaacaacagctcactgtggtcaattctatgcatctgacatccaatattct	689
Db	544	TTACGCGCTTAAAGAACGATTTGACGGGGCCAAATCCCTAGAGACTCATGTGCAATCCCA	603
OY	690	acccttcaagtttgatctatcatcaataacagacctctcgtgctagcttcctgacatgac	749
Db	604	AGCCTTAAAGTTGTGATGATCTCAAGCAATGATTTGTGTGGGAACATCCCAACAAACGA	663
OY	750	tcctctcactcttcacaccatcactgatttgctaaataac	788
Db	664	CCTTTTGCTCACATTCCTTTACAGAATCTTGAGAACAC	702
RESULT	7		
ID	V06587		
AC	V06587	standard; cDNA to mRNA; 981 BP.	
DT	03-AUG-1998	(first entry)	
DE	Arabidopsis thaliana	SERK LRR homologous EST clone.	
KW	receptor kinase; apomixis; apomixis; seeds; production; embryos;		
OS	Arabidopsis thaliana.		
FT	key	location/Qualifiers	
FT	CDS	104..760	
FT	FT	/tag= "a	
FT	PN	/note= "shows high homology to SERK"	
PD	WO9743427-A1.		
PF	20-NOV-1997.		
PR	13-MAY-1997; E02443.		
PA	14-MAY-1996; GB-010044.		
PI	(NOVS) NOVARTIS AG.		
DR	De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;		
DR	WPI; 98-086529/08.		
PT	P-PSDB; MA7019.		
CC	Production of apomictic seeds - useful in plant breeding		
CS	Claim 28; Pages 75-77; 12pp: English.		
CC	The sequence is that of an EST clone showing high homology to		
CC	SERK LRR (leucine-rich repeat) sequences.		
SC	Sequence 981 BP; 286 A; 236 C; 180 G; 279 T;		

Query Match	10.1%	Score 211.8;	DB 1;	Length 1063;
Best Local Similarity	63.0%	Pred. No. 2,3e-49;		
Matches 327; Conservative	0;	Mismatches 197;	Indels 0;	Gaps 0;
Sequence 1063 BP;	313 A;	242 C;	206 G;	302 T;

	Query Match	10.1%	Score 210.2	DB 1	Length 981
	Best Local Similarity	62.8%	Pred. No. 6.2e-497		
	Matches 326	Conservative	0	Mismatches 193	Indels 0
					Gaps 0
QY	270	gctaatttgaagtgatgctttgcataactttgagggatctactgattgatccaacaat	329		
DB	182	GCAAATCTCGAAGGAGATCTCTTACAGCTCTTCCCGAGATTTCACGATCAACACCAT	241		

Oy	471	aagaatttcgaagattttgagcttcaacagtaacaacataacgagccgcatctccagtaat	530
Db	1401	GAGCATCTTCTCAAGATGAACTTGACTACAAATACATATACCTGGGTAGTTCCAGGGCAC	1460
Oy	531	cttggaaatctgcacaactctagtagtcttgatctcttaacttaaacagctctccgctct	590
Db	1461	TTTGGAAATCTTAAGAAAGCATCATGAAATAAGATCTTTCAAATAATAGATATCTGGGCCA	1520
Oy	591	attccggaatcatttgggaaagcttcaaaagctcgagatcttccggtttaaacaacaacagt	650
Db	1521	ATWTCACAAAGCTTAACCATATTCAGAAACATTAATTTTGCTAGACTGGAAAAATATATAC	1580
Oy	651	ctcacgtgctcaatcccatgctacgcgacaatatattacacctcaagttcttagatcta	710
Db	1581	CTGACGTG---TATGTGTGGTTTATTAGCCAACTGCTCAGTCTCAGCTATTTGAATGTA	1637
Oy	711	tcaataacagactctctggtctcagttccctgcgaatgctctctcactcctcaacacc	770
Db	1638	TCTCATATCAACCTCGTAGGTGTATCCCTTAAGAACATTAATCTTCCACAGATTTTCACCA	1697
Oy	771	atcagtttgctaaacttagaccatcttgaaacctgttaaacgtaaccacagctgcgcga	830
Db	1698	GACAGCTTCATTTGGCAATCTGTGCTTTTCGGTAGTGGCTTAACCTCACCGTGCATGAT	1757
Oy	831	tctcccccgtttctctccacacacctttattcaacactcccccaagtttccaccccagat	890
Db	1758	TCCTC-----GTCGAACGTACGAGTGCATCTCTCTAGA	1790
Oy	891	gggtatggtataactgaggaataagctg--tggagttgtcgaagtgtcgtcttgccct	948
Db	1791	GCACCTATTTCTTGGAATAGCTATTTGGGGGCACTTGATCTCTCTCATGCTTAATATGCA	1850
Oy	949	tgtgtgtccctgcgaatagcctctgtctgtgtgtggtgcgaagaagcccaatagatatctct	1008
Db	1851	GCTTGGCGAOCGATATCTCCTCCTCTTTTCTTGATGATCATCTTGACAAACCGATACT	1910
Oy	1009	tcgatgtccctgcgcgaagaagatccagaagttcatcttggagacgtctcaagaagtttctt	1068
Db	1911	TATTCGACACCGAAGCTCGTCACTCTTCATATGAATGACGACCTC-----CACGTTT	1962
Oy	1069	tgcgagagctcaagaigtgcgagtgatgaggttttagtaacaagaacatttggcgagaagt	1128
Db	1963	ACGAGGATATCATGAGAATACAGAGAAATCATAGTGAAGAATATTCATTGGCGACGAG	2022
Oy	1129	ggtttggaaagcttcaagaagsgcgttgcgcagacggaactctgtgtcgtcgaagagac	1188
Db	2023	CATCAACACACTGATACAAATGTGTTTGAAGAAATGTAAACCGGTTCGATTAAGCGGC	2082
Oy	1189	tgaaggaagagcgaactccaggtgtggagagctcgaagttaacaacagaatlaagatgataa	1248
Db	2083	T---TTACTCTCACACCACCACTCAATGATAAAGTTTAAACAACACTCGAGATGCTAA	2139
Oy	1249	gtatgtagcttcatcgaaaactgtttagatctacgaagttctcgtatgtaacacgcagcaga	1308
Db	2140	GTACGATCAACAGCAAGAAATCTGTGAGCCTCAACACTTATCCCTCCTCACTTGAGGA	2199
Oy	1309	gattgctgtgtatcctctaaatgyccaatggaagagtgtctcgtgtccagagagagac	1368
Db	2200	GTCCTTGCTTATGACTATTTTGGAAAAATGTAGCCTC--TGGAGCTTCTTCATGCGCC	2256
Oy	1369	cacgtcacaaacctccgctgattgtgcacagcgagaagaatcgcgtctagctcaagtc	1428
Db	2257	CTACGAAAGAAAAGACTCTTGATTTGGGACACACGCGTTAAATACATATGTTGTCAGAC	2316
Oy	1429	gaggtttgcttactacatgatcactgcgcatccgaagaatctcacogtgcgtaaaag	1488
Db	2317	AAGGTTTAGCTTATCTACACCATGATGTAAGTCAAGATCATTTACAGAGACGCTGAAGT	2376
Oy	1489	cagcaacaatccctcttagaagaagaatttcgaagcggtgtgtggaatttcggtgttgaa	1548
Db	2377	CGTCCACATCTCTTGTGGACAAAGACTGTAGAGGCTCTGTTGACAAATTTTGGAAATAGCGA	2436

[illegible]

RESULT 10

JD X23531 standard; cDNA: 3045 BP.
 AC X23531;
 DT 17-JUN-1999 (first entry)
 DE Maize xal21 gene D14 cDNA fragment.
 KW xal21; receptor kinase-like protein; multigene family; RRK; rice; DT4;
 KW plant disease resistance; cassava; maize; tomato; Xanthomonas; ss.
 OS Zea mays.
 PN M09909151-A2.
 PD 25-FEB-1999.
 PF 17-JUL-1998; U14841.
 PR 13-AUG-1997; US-910386.
 PA (REGC) UNIV CALIFORNIA.
 PI Hubert SH, Richter T, Ronald PC, Song W, Szabo V,
 PI Wang G.
 DR MPI: 99-204431/77.
 NR New RRK polynucleotides and nucleic acid constructs - used for
 PR generating transgenic plants resistant to Xanthomonas
 PT Claim 12: Page 58-59; 67pp; English.
 PS Claim 12: Page 58-59; 67pp; English.
 CC This invention describes a method for conferring disease resistance in
 CC plants. The invention describes the use of novel genes and proteins
 CC belonging to the Oryza longistaminata and Oryza sativa receptor
 CC kinase-like protein (RRK) xal21 multigene family. Such genes from
 CC cassava, maize and tomato are also described. The genes and proteins can
 CC be used for enhancing resistance to Xanthomonas in a plant, preferably in
 CC rice or tomato.
 SQ Sequence 3045 BP; 717 A; 739 C; 744 G; 735 T;

Query Match	7.7%;	Score 160;	DB 1;	Length 3045;
Best Local Similarity	52.68;	Pred. No. 1.1e-34;		
Matches 449;	Conservative	0;	Mismatches 386;	Indels 18;
				Gaps 4;

QY	1075	agtaacaagctggcagatgaggttttaataacaagaacatttggcacaagcttgagttg	1134
Db	1946	ACCTGCATGAGGCTACCAATAGGCTTACGCTCGGAACCTTTGTTGGCAGAGGATTCG	2005
QY	1135	ggaagcttaacaaggaagcgtttgcagacggaactctgttgcgttcaagagactgaag	1194
Db	2006	GTGAGGTTTACCAAGCTAGAGCTCATGATGAGCGAGCTTGCTGCCTGCAAGANCTGATGC	2065
QY	1195	aagagcgaactccagatggcagagctcgafttcaacaagaatgaagatgaatatg	1254
Db	2066	ATTTCACAGGCCAAGGC---GACGGGAGGTTCACTGCAGATGAGAGACATTGGCAAGA	2122
QY	1255	cagttcaatcgaaacctgttgaataacgaagttctgtatgaacacgagcgaagatgac	1314
Db	2123	TCAAAACATCGCAACCTTGTCGCGTGTAGGTAATGCAAAAGTTGGCGACGAACTGTC	2182
QY	1315	ttgtgtatccttacaatgccaatggaagatgttgcctcggtctcagaagagagccacgt	1374
Db	2183	TTTGCTGTACGACTACATCATATATGGAAGCCGTGATGTCTTGTCCCATGAAGAAGCAAGA	2242
QY	1375	cacaacctcgcgtatgtatggccaacgcsggagaagaatcgctgaagctcagctcgaagt	1434
Db	2243	CTGATGTGGGCTTGATTTGGGCAACAAGAAAGATTGCAATGGCTGCGCAAGAGGAC	2302
QY	1435	tgcttactacatgatcactgacatccgaagatcatcacaacgttgaacgctgaagaacga	1494

Db 2303 TGGCTTCCTCCACCAATGTCATCCCAACATCATACCGGAGCATGAATCAAGCA 2362
QY 1495 acatcctcttaagcagaagattcgaaagcggttttggaatttcgggttgccaactta 1554
Db 2363 ACCTGCTCTTGTGACGAATATCTGATGCCCTACCTATCGAATTTGGAAAGCGCGCTCG 2422
QY 1555 tggactataaagcacatcagctgac---aacagcagtcggtgcacatcgctacatcg 1611
Db 2423 TGAATGCTGTGACTCACAATCTAACCGTGAAGACTCTTAAAGAACACTGGTATGTGG 2482
QY 1612 ctccagaatactctcaaccggaaactctcagagaacacgacgcttttcgatacgaa 1671
Db 2483 CTCCCAAGTACTCTCCAGTGGTATTGTGCAACAACCTAAGGCGCACGCTACAGCTATGGCG 2542
QY 1672 tcatgtcttaagactcaatcaacgagaagactttgatctcgctcgctagctaaag 1731
Db 2543 TTGTTCTTCTGGAGCTTCTCTCAGGGAAAAAACCAATCAATCCGACTGAAAT----- 2595
QY 1732 acgacgacgtcatgttacttgactgggtgaagagattgttgaagagaagaagctagaga 1791
Db 2595 -CGGCGACAAATATCTCATCGACTGGGCGCAAGCAGATGGTTAAGAGAGACCGGTGCAGCG 2653
QY 1792 tgttagtgcatacagatcttc---aacaactacgagagagaagactggaacaaatga 1848
Db 2654 AGATATTTTGATCCTTATTTGACCGCACAAAAATCTGCGAGTGCAGCTGTACAGTATC 2713
QY 1849 tacaagtgcgttgcctatgcacgcaagatcaccaatggaagaaccaaagatgctgaag 1908
Db 2714 TGGCGATGCTTGCCAGTGGCTTGAGACATCAACCTAGTCGACACCTACAGATGATCCAG 2773
QY 1909 ttgtaagagatgct 1921
Db 2774 TCATGGCAATGTT 2786

RESULT 11
X23533
ID X23533 standard; DNA; 3842 BP.
AC X23533:
DT 17-JUN-1999 (first entry)
DE Tomato Xa21 clone TRK2 DNA fragment.
KW Xa21; receptor kinase-like protein; multigene family; RRR; rice; TRK2;
KM plant disease resistance; cassava; maize; tomato; Xanthomonas; ss.
OS Lycopersicon esculentum.
PN M0909151-A2.
PD 25-FEB-1999.
PE 17-JUL-1998; 014841.
PR 13-AUG-1997; US-910386.
PA (REGC) UNIV CALIFORNIA.
PI Hulbert SH, Richter T, Ronald PC, Song W, Szabo V,
PI Wang G;
DR WPI; 99-204431/17.
DR P-PSDB; W23533.
PT New RRR polynucleotides and nucleic acid constructs - used for
PT generating transgenic plants resistant to Xanthomonas
PT Claim 14; Page 61-62; 67pp; English.
CC This invention describes a method for conferring disease resistance in
CC plants. The invention describes the use of novel genes and proteins
CC belonging to the Oryza longistaminata and Oryza sativa receptor
CC kinase-like protein (RRK) Xa21 multigene family. Such genes from
CC cassava, maize and tomato are also described. The genes and proteins can
CC be used for enhancing resistance to Xanthomonas in a plant, preferably in
CC rice or tomato.
SQ Sequence 3842 BP; 984 A; 719 C; 894 G; 1244 T;

Query Match 6.8%; Score 142.6; DB 1; Length 3842;
Best Local Similarity 46.0%; Pred No. 8.6e-30;
Matches 682; Conservative 0; Mismatches 774; Indels 25; Gaps 5;

QY 459 ctgtgtgtcctcaagaatttcagattttgagctttacagtaacacataactgcccg 518
Db 2039 CTGGCCAGATTAAGGATCTCACTTCTCTTGGCTGGCAATTAATCTGGTGGCCCA 2098

QY 519 attcctagtaatttggaatactgacaaactagtgagtttgatcttacttaaacagc 578
Db 2099 ATCCCTCAAGTTTGGCCAAATTCACCTTTGAGAAAGCTTTGAACTTTCTGCAATTC 2158
QY 579 tctccgggtccattccggaatcattggaaagcttccaagctgagattctccggct 638
Db 2159 TTGCTGGGTGAATTCGAAATTAATCTGTAATTTGAGAAATTTGACTCTCTTCTCTG 2218
QY 639 aacaacaaagctcactggttcaaltccatgltcaactgacaaatatactaccctcaa 698
Db 2219 AACACAACAATTTATTCAGGGAATAATACCTTCAGGCTTGCCAAATGAGACACACTGCA 2278
QY 699 gtgttagatcatacaataacaagactctcggttcagttccttgacaaatgctccttca 758
Db 2279 GCATTTAAGTTTCTTTCAATTAATCTGTCTGGCCACTGCTTCAACAAAGATTTATG 2338
QY 759 ccttcacacccatcagtttgcataataactagaccatgtgaccctgttacagatcac 818
Db 2339 AAGTGTAAATAGTGTTCAGGGAAACCCCTTTCTGCAATGTCCTCATGATTTTCTCTATCA 2398
QY 819 ccaatgctcgtgactcctcccg-----tttctcctcacaccctttatccaactccc 872
Db 2399 ACACCTTCTACAGATCACAGGGAAGATAGGGACACTCAAGATTCGTGCGTCTCCT 2458
QY 873 ccaagttccaccccgagtggtatgtaactg-----gagcaatactggtgga 923
Db 2459 TCAAGTTCAACCCAGAAAGAGGAGGAGCGAGCTTCAACTCCATTAAGATGATGCCATA 2518
QY 924 gtgtcgtcagtgctgcttgccttgcctcgtcctcgtcaatagacttgcgttggtgcga 983
Db 2519 ACATCTCGGCGCAGCTATGTGTGCTGCTTCTGCTGCTGATAGTCGTCGTTTAAACC 2578
QY 984 cgaagaagcccaactagatatcttctcgatgltccctgcggaagaatccagaagttcat 1043
Db 2579 AGAAATGGAATCCAAGATCTAGAGATTCGTGATCTACAGGAAGAAAGTCACAGTGTTT 2638
QY 1044 ctggaacagctcaagaagtttcttcttgcgagagcttacaagtggcgagtgtatgattagt 1103
Db 2639 ACAGAAGTTCGGGTTCTTTTAAATGAAATGTAGTCGGGCGCACAGGAGCTTCAAT 2698
QY 1104 aacaagaacatttggcgagagtggttgggaagactcaagaggaagcttgagagac 1163
Db 2699 GCACCAATTCGATAGCGCAGTGGAGGTTTGGAGCACATACAAAGCGGAGATTGCACCA 2758
QY 1164 ggaactctgttctgltcaagaagactgaagaagaagcgaactccaggtggaagctccag 1223
Db 2759 GGGTTCCTAGTGGCAGTAAGCGACTTGTGTAGGAGCTTTTC--AGGGATTCACACAG 2815
QY 1224 ttcaacaagaagtgaagatgataatgtagcaagttcaatcgaaacctgttgatitcga 1283
Db 2816 TTTGATGCGAAGAAATCAGAACTGGGGAGGCTTCGACATCCAAACCTCGTAACCTGATA 2875
QY 1284 gttctctgtagaacacgacagagagattgcttgtgtatcccttaacatgagcaatggaagt 1343
Db 2876 GCATTTCAATATAGGAACACGAATGTTTCTGATCTTAATCTATTTGCCAGGTGTAAT 2935
QY 1344 gtgtcttgltctcaagaagaagccacagctcaaacactcgcgttgatgccaacgcg 1403
Db 2936 TTGGAAGATTATTCAGAGAG-----GTCACAAAGGCGGTGAGACTGAGGGTTCTT 2989
QY 1404 aagagaatcgcgttaggtcagctcgtcgagtttgttcttaactaataatgatactgcgtcg 1463
Db 2990 CACAAGATTGCTTTGGATGTAGCCGTCCTACCTTGACCTGCAATGATGATGTGTACCA 3049
QY 1464 aagatcatcaccgtgagcgtaaagaagcagaacatcccttaagcagaagaattcgaagcg 1523
Db 3050 CGTGTGCTTTCATCGATGTGAAGCCGACGAACATTTTATTTGATGAGAGATTAATGCA 3109
QY 1524 gtgttgagaaatttcgggttgcaagcttattgactataaagaacacactcgtagacaca 1583
Db 3110 TATTTATCTGAATTTGGTTGGCTAAGATTTACTGGGAACCTTAGAGACCCATGCAACTACT 3169

QY 1584 gcagtcctgagccatcgctacatcgctccagaaatctctcaaccggaaatcttca 1643
DB 3170 GGTGTGGGGGAACCTTTGGATGTTGCTCTCGAATATGCCATGACTTCCGGCTTCG 3229
QY 1644 gagaacacgcagcttttcgatacgaatcatgctcttagaactacacagagacaaga 1703
DB 3220 GACAGAGGTGATGCTACAGTATGAGGGTGTGTTGCTTGAATATCATGATTAACAAA 3289
QY 1704 gcttcgatacgcctcgagtagctaacgacgacgacgtcatgttacttgactggtgaa 1763
DB 3290 GCATAGATCCGCTTCTCTCTTATGAAATGATTCATATTTAGCTTGGGCATGC 3349
QY 1764 gactgttgagagagaaagctagagatgtagtgatccagatcttcaacaactac 1823
DB 3350 ATGCTTTTACCGAGCGCCGCTTACGAGATCTTTACGCTGCTCTTGGATTCAGTTC 3409
QY 1824 gaggagagagaaactggaacaaatgatacaagtggcgttgcatacgcgaagatcacca 1883
DB 3410 CACATGAT-GATTTGATGATGAGTCTCTACACTTGCAGTGGTCTGACGTTGACTCTT 3468
QY 1884 atggaagaccaaagaatgctgaagtgtgaagtgtgaa 1924
DB 3469 TCTACTAGACCAACATGACAGTATGAGACGTTGAA 3509

RESULT 12
X07356
ID X07356 standard; DNA; 4104 BP.
AC X07356;
DT 21-MAY-1999 (first entry)
DE Arabidopsis steroid receptor Bin1 DNA.
KW Bin1; steroid receptor; receptor kinase; transgenic plant;
KM brassinosteroid; disease resistance; crop protection;
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 97..3687
FT CDS /*tag= a

MO9859039-A1.
PD 30-DEC-1998.
PR 24-JUN-1998; U13100.
PR 24-JUN-1997; US-881706.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
PI Chory J, Li J;
DR WPI: 99-081275/07.
DR P-PSDB: W97819.
PT New receptor kinase Bin1 involved in brassinolide signalling -
useful for promoting increased yield and disease resistance in
PT plants and for modulating oocyte maturation
PS Claim 8; Page 49-52; 72pp; English.
CC This DNA sequence codes for a novel plant steroid receptor kinase,
designated Bin1 (see W97819), which is involved in the pathway for
CC the synthesis of the plant steroid hormone, brassinolide. 18 New
CC Arabidopsis dwarf mutants were identified that lacked the ability
CC to respond to brassinolide, and were named bin mutants. The bin1
CC mutations were used to map the gene to a small interval on
CC Arabidopsis chromosome 4. Bin1 was cloned by map-based cloning.
CC The bin1 polynucleotide was identified within this interval by
CC sequencing the wild-type and mutant alleles of this nucleic acid.
CC Overexpression of Bin1 in transgenic plants provides plants
CC characterised as having enhanced disease resistance, increased
CC plant yield or vegetative biomass and increased seed yield.
CC Expression of Bin1 may also increase resistance to pesticides.
CC Inhibition of Bin1, e.g. using antisense oligonucleotides (AON), is
CC used to render plants male-sterile, and to reduce their stature or
CC yield, e.g. for creating dwarf varieties. Since Bin1 homologues
CC may be involved in regulation of the menstrual cycle and uterine
CC function, Bin1, antibodies and AON may be useful as contraceptives,
CC for improving success of in vitro fertilisation and to prevent
CC premature labour. Transgenic animals are also provided, and are
CC models for studying steroid-receptor interactions or can be used
CC to screen for therapeutic agents.
Sequence 4104 BP; 1061 A; 870 C; 930 G; 1243 T;

Query Match 6.7%; Score 139.6; DB 1; Length 4104;
Best Local Similarity 52.9%; Pred. No. 6,1e-29;
Matches 348; Conservative 0; Mismatches 304; Indels 6; Gaps 2;
QY 1058 gaagttcttcttcgagagctacaagtgagtgagtggttagtaacaagaacattt 1117
DB 2703 GAGGCTCACGTTTGGCGATCTTCTTACAGCTACCAATGTTTCCATATGATAGCTCAT 2762
QY 1118 gggcagaggttggttttggaaagctacaaagagcgttggcagacggaactctgttc 1177
DB 2763 TGGTTCTGGGGGTTTGGAGATGTTTACAAAGCATTTTGAAGATGGAAGCGCGGTGGC 2822
QY 1178 tgtcaagaagctgaagaagaagcgaactcaagtgagagagtcctccagtttcaacgaagt 1237
DB 2823 TATCAAGAAATCTATTCATGTTAGCGCTAAGT--GATACAGAGTTTCAAGCGGAGAT 2879
QY 1238 agagatgataagratgagcaagttcatcgaacctgttgaattagcagagttctgtatgac 1297
DB 2880 GGAATCATTGGGAGATATCAACATCGAAATCTTGCTCTTCTTGGTTATTCGAAAGT 2939
QY 1298 accgacgagagatgtctgtgtatccttacatggccaatggaagtgctgtct 1357
DB 2940 TGGAGACGAGCGGCTTCTGTTAATGAGGTTATGAAGTATGGAAGTTAGAAATGTTT 2999
QY 1358 cagaagagagccacgcgtcaacaacctcgttgattggccaagcggagagaatcgctt 1417
DB 3000 GCAAGACCCCGAAGAAAGTGGGGTGAAACTTAAATGTCTCACACGCGGAGATGGCAT 3059
QY 1418 aggcatagcctcagagttgttcttaccatcatcactcgcatacgaagatcatcacg 1477
DB 3060 AGCATATCAGCTAGAGGGCTTCTTCTTCCACCAACCTGCAATCCGCAATATCATCACAG 3119
QY 1478 tgacgttaaaagcagaacaatccctcttagaagaagaattcgagcgtgtgtgagatt 1537
DB 3120 AGACATGAATATCCAGTAATGTGTGCTTGATGAGATTTGGAAGTTCGGGTTTCAGATT 3179
QY 1538 cgggttggcaagactatgactataagaacactcaacgta--caacagcgttcgtag 1594
DB 3180 TGGCATGGCGAGGCTGATGATGCTCGATGATAGCGCATTTTAAACGCTACAGTATGCTGG 3239
QY 1595 caccatcgctacatcgctccagaatatctcacaacggaaaactctcagagaagaaccca 1654
DB 3240 TACACCGGTTACGTTCCCTCCACAGATATTACCAAGTTTACAGGTGTACAAAGAGGA 3299
QY 1655 cgtttcgatacgaatacgtctcttagaactaatacagagacaagaagcttgcatt 1712
DB 3300 CGTTTATGATTACGGTGTGTGTTTACTCTGAGCTACTACGCGGTAAACGCGCCAAACGAT 3357

RESULT 13
T31307
ID T31307 standard; cDNA; 1554 BP.
AC T31307;
DT 15-NOV-1996 (first entry)
DE Tomato RRK gene clone TRK1.
KW Xa21; RRK; disease resistance; Xanthomonas; blight; rice;
KW tomato receptor kinase 1; TRK1; transgenic plant; crop protection;
KW ss.
OS Lycopersicon esculentum.
PN MO9622375-A2.
PD 25-JUL-1996.
PR 17-JUN-1996; U00717.
PR 17-JUN-1995; US-373374.
PR 07-JUN-1995; US-475891.
PR 29-SEP-1995; US-004645.
PA (REGC) UNIV CALIFORNIA.
PI Ronald PC, Song W, Szabo V, Wang G;
DR WPI: 96-354532/35.
DR P-PSDB: W03186.
PT Plant disease resistance gene Xa21, codes for RRK polypeptide -
useful for conferring resistance to Xanthomonas in rice and tomatoes

PT DNA encoding plant morphogenesis regulatory protein - useful to
PT yield plants with short stems or altered inflorescence
PS Claim 6; Pages 12-15; 17pp; Japanese.
CC The present sequence encodes an Arabidopsis thaliana plant
CC morphogenesis regulatory protein (MRP), which can be used to yield
CC a plant with, e.g. short stems or altered inflorescence. The MRP
CC acts on a plant at a specific site for a specific period, and can
CC therefore be used to regulate extraneous gene expression in a
CC plant. The MRP's cDNA or genomic DNA can be used to transform a
CC plant to increase its MRP expression, and therefore control the
CC form (particularly stem length) of the plant.
SQ Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;

Query Match 5.5%; Score 114.4; DB 1; Length 9295;
Best Local Similarity 56.7%; Pred. No. 9.8e-22;
Matches 211; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 1345 ttgcttcggtctcagagagagccacgctcacacctccgcttattggtccaaagcgga 1404
DB 6499 ttcccttgggtgtttttaaagccctacagagaaaaagaccttgaattggacacacggc 6558
QY 1405 agagaatcgcgtcagagctcagctcgaggtttgcttacctacatgatcactgcgattccga 1464
DB 6559 tttaagattacatattggtgacgacacaggttttagcttattctacacatgactgtattccaa 6618
QY 1465 agatcattcacggtgacgtaaaagcagaacatcctcttaagcgaagaattcgagcg 1524
DB 6619 ggatcatttcacagagacgtgaagtcgtccacattcttggacaaagaccttaagagcgtc 6678
QY 1525 ttgttgagatttcggggttcggaagcttaagactataaagacactcagtgacacag 1584
DB 6679 gtttgacagatttttggaatagcgaagaaagcttgggtgttcaaaagtcacatcttcaactt 6738
QY 1585 cagtcggtgacccatcgttcacatcgttcagaatattctcaacggaanaattctcag 1644
DB 6739 acgtgatgggacagatagattacatgacccagatattctgcacttcacaggtcactcg 6798
QY 1645 agaaacccgacgttttcgatacgaatcatgcttctagaactaatacagaagacaagag 1704
DB 6799 agaaatccagatgtctacagtattgaatagtccttcttgattgttaaccgaagaaag 6858
QY 1705 cttcgattctcg 1716
DB 6859 ccgtgatgacg 6870

Search completed: June 23, 2000, 22:54:50
Job time: 40686 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 19:06:46 ; Search time 6198.48 Seconds
(without alignments)
1366.010 Million cell updates/sec

Title: US-09-180-798-32
Perfect score: 2089
Sequence: 1 ggattttattattttttt.....taaaaaaaaaaaaaaaaaa 2089

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
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8: em_est8:*
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107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OY	1669	atcaagaagaaaggcttgcgattcgttcgtcgtagctaagaagacgaactcaagtta	1748
Dd	658	gtccactgtgcaccggagcccatatgacctttttcacgcttg--acgaagaaatgatgtgtta	714
OY	1749	cttgacgtggttaaaggatttgttaagaagaaagctagaatgttaagtatccagat	1808
Dd	715	ctttgattcatgtacaacacctgcmaaaggagggcattctgacgccattattgacctaac	774
OY	1809	ctccaacaactacgagagagagaacttgyaacaagtatacaagtgcgttatgc	1868
Dd	775	ctgaacaacaaatttacacagcgagcagagagtgagatgatgatccagatccgctctgc	834
OY	1869	acgcaagaatcaccccaatgyaagaaccaaatgcttgaagttgaagatgcttgaagga	1928
Dd	835	acgcagagccttcccctcgagagaccggcgtccatctccgaagtgctccggtcggaagcc	894
OY	1929	gatggagcttgagagaaaatgtagcaatgycgaacaaagttagagatttgag	1979
Dd	895	gagggccttcgcagagagctggagagagtgccagcagcttgagctgacgag	945
RESULT	2		
AA738547			
LOCUS	AA738547	656 bp	mRNA EST 17-AUG-1998
DEFINITION	SbRLK5 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone SbRLK5 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.		
ACCESSION	AA738547		
VERSION	AA738547.1	GI:3421472	
KEYWORDS	EST.		
SOURCE	sorghum.		
ORGANISM	Sorghum bicolor		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllopes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.		
AUTHORS	1 (bases 1 to 656)		
TITLE	Annen,F., Chang,J.-L., Paterson,A.H. and Stockhaus,J.		
JOURNAL	Characterization of 14 different putative protein kinase cDNA clones of the C4 plant Sorghum bicolor		
MEDLINE	Mol. Gen. Genet. 259 (1), 115-122 (1998)		
COMMENT	98409267 On Nov 29, 1993 this sequence version replaced gi:636097. Contact: Stockhaus J Institut fuer Entwicklungsbilogie und Molekularbiologie der Pflanzen Heinrich-Heine-Universitaet Universitaetsstrasse 1, 40225 Duesseldorf, Germany Tel: (49)-211-81-14953 Fax: (49)-211-81-14871 Email: stockha@uni-duesseldorf.de		
FEATURES			
source	Insert Length: 1100 Std Error: 0.00. Location/Qualifiers 1..656 /organism="Sorghum bicolor" /strain="cv. TX430" /db_xref="taxon:4558" /cclone="SBRLK5" /cclone_lib="Sorghum bicolor cv. TX430 leaf" /dev_stage="green" /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Eco RI site_2: Xho I; leaf cDNA library from green leaves, unidirectionally cloned"		
BASE COUNT	161 a 145 c 184 g 166 t		
ORIGIN			
Query Match	17.3%:	Score 360.6;	DB 38; Length 656;
Best Local Similarity	73.0%:	Pred. No.1,7e-82;	
Matches	478; Conservative	0; Mismatches 174;	Indels 3; Gaps 1
OY	1279	tacggagttctgtatgaacacgacgagaaattgctgtgtatccttaccatgagcaatg	1338

Db	2	TTCTGGGTTTTCGATGATGACGCCCTTACTGACGGTTGCTACTGATCAACCATATCAGNGCCTAATG	61
QY	1339	gaagltgtgtcttctgtctcagaagagagcgacccgtcaaacctcccgcttga---c	1395
Db	62	GGAGTGTGCATCAGTTTACGAGAGGACAGCAATCTGAGCCACTGTTAAGTGGGAAA	121
QY	1386	caacgcggaagaagaatcgcgtcgaagctcaagctcgaagtttgccttaacctatgacct	1455
Db	122	CAACCAAGAAAGACGGATTGGCGCTTGGATGTCAGAGAGACTTCTTACTTGCAATGATCACT	181
QY	1456	ggcgtccgaagaatattcacccgtgaagtaaaacacgaacatccctcttagcgaagaat	1515
Db	182	GGGATCCCAAAATATATCATGTGGGATCTCAAACTGCAAATATCTTCTTCAGAGACT	241
QY	1516	tcgaagcggttgttggaatttcgggtctggccaagctatagactataaagaacactcacg	1575
Db	242	TGAGGCGAGTGTGGGGATTTTGGGCTTCCCAAGCTTATGAGCATCAAAAGATACCATTG	301
QY	1576	tgaacaacagcttcgctgtgaacatcgttcacatcgtctccagaatactctcaacggaa	1635
Db	302	TCACAACTGCTGCTCCGTTGAAACAATTGACACATTCGCGCTGAGTCACTATCCATGGCA	361
QY	1636	aattctcaagagaanaacggaogttttcggataaagaaatcattgtctcttagaactaatcacag	1695
Db	362	AGTCCTCTGAAAACATGATGATTTTGGCTATGGATCAATGCTTCGTGGAGCTTATTACTG	421
QY	1696	gacaaagagcttcgcatctcgtctcgctgaagctaaacagacgacgctcagttaactgact	1755
Db	422	GCCAGAGGGCATTTGATCTTGCTGCTGTTCCAAATGATGACATGTATGCTTCTTGACT	481
QY	1756	gggtgaagaagattgttgaagagaagaagctagaagatgttaagtgaatccagatcttcaaa	1815
Db	482	GGGTGAAGAGCATGCTGTAAGAGACAGAGGTGGAGATGCTGGTGGAGCCACAGATCTGCAGA	541
QY	1816	caactcagagagaagaggaacttggaaacaagtatacaagtggcggttgcatacgaacgcaag	1875
Db	542	ACGCTTACGAGAGATGTCAGGTGGAGAACCTGATTCAGGTGGGACCTCTTCACGACGAG	601
QY	1876	gataccacatggaagaccaaagaatgtcctaagtttgaagatgactcgtgaagaga	1930
Db	602	GCTCCCGTTTGACTCTCCCAAGATGTCGAGGTGGTGTGAGAGTCTCGAAGGTGA	656
RESULT	3		
AA738545			
LOCUS	AA738545	1435 bp	mRNA
DEFINITION	SBRLK1 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone	EST	17-AUG-1998
	SBRLK1 similar to protein kinase, highest similarity to		
	receptor-like protein kinases, mRNA sequence.		
ACCESSION	AA738545		
VERSION	AA738545.1	GI:3421470	
KEYWORDS	EST.		
SOURCE	Sorghum.		
ORGANISM	Sorghum bicolor		
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;		
	Poaceae; Sorghum		
REFERENCE	1 (bases 1 to 1435)		
AUTHORS	Annen,F., Chang,J.-L., Paterson,A.H. and Stockhaus,J.		
TITLE	Characterization of 14 different putative protein kinase cDNA		
	clones of the C4 plant Sorghum bicolor		
JOURNAL	Mol. Gen. Genet. 259 (1), 115-122 (1998)		
MEDLINE	98409267		
COMMENT	On Nov 29, 1993 this sequence version replaced gi:636085.		
	Contact: Stockhaus J		
	Institut fuer Entwicklungsbiologie und Molekularbiologie der		
	Pflanzen		
	Heinrich-Heine-Universitaet		
	Universitaetsstrasse 1, 40225 Duesseldorf, Germany		
	Tel: (49)-211-81-14953		
	Fax: (49)-211-81-14871		
	Email: stockhae@uni-duesseldorf.de		

[illegible]

DB	1271	TCCTTCGACGAGGCTTCGCTTGAAGGACCGGCGCTTCATGTCGAGGTGGTCCGGAATGC	1330
OY	1921	tggaagagatgggtgttcgcggaagaattggacgaatggcaaaaattgagatttgagg	1979
DB	1331	TGGAAAGCGAGAGCGCTTCGACGAGAGGTGGAGAGTGGCAGCAGCTGGAGGTGACGAGG	1389
RESULT	4		
LOCUS	A1728030		
DEFINITION	A1728030	555 bp	mRNA EST 11-JUN-1999
ACCESSION	BNGH19629	six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U93048) somatic embryogenesis receptor-like kinase [Daucus carota], mRNA sequence.	
VERSION	A1728030		
KEYWORDS	A1728030.1	GI:5046816	
SOURCE	EST.		
ORGANISM	upland cotton.		
REFERENCE	Gossypium hirsutum		
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicots; Rosidae; eudicotyledons; core eudicots; Malvales; Malvaceae; Gossypium.		
TITLE	1 (bases 1 to 555)		
JOURNAL	Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.		
COMMENT	ESTs from developing cotton fiber unpublished (1998)		
	On Jun 5, 1998 this sequence version replaced gi:3187310.		
	Contact: Ben Burr		
	Biology Department		
	Brookhaven National Laboratory		
	Upton, NY 11973, USA		
	Tel: 516-344-3396		
	Fax: 516-344-3407		
	Email: burrdnluxl.dnl.gov		
	Seq primer: T3 Primer.		
FEATURES	location/qualifiers		
source	1..555		
	/organism="Gossypium hirsutum"		
	/cultivar="Acala Maxxa"		
	/db_xref="taxon:3635"		
	/clone_lib="Six-day Cotton fiber"		
	/issue_type="Immature fiber"		
	/dev_stage="Six days post anthesis"		
	/lab_host="XLI-Blue"		
	/note="Vector: pBluescript II KS+"		
BASE COUNT	146 a 100 c 147 g 162 t		
ORIGIN			
Query Match	16.3%, Score 341.4; DB 51; Length 555;		
Best Local Similarity	76.2%; Pred. No. 1.4e-77;		
Matches 420; Conservative	0; Mismatches 131; Indels 0; Gaps 0;		
OY	1522	cggtgttgtagagattcggtgttggaagctatagactaaagaacctcagtgcaaa	1581
DB	1	CTGTTGTGGTACTTGTGGGTGGCTTAACCTATGAGACTACAAAGATACCCATGTAACTA	60
OY	1582	cagcagctcggtgacacatcggtccacatcggtccagaatatctccaacgcggaatatct	1641
DB	61	CTGCTGTACGTGGCACAATTTGACACATATTGCTCCGTGAGATGTCCTTACTGSAANAATCTT	120
OY	1642	cagagaaaaacgcagcttttcgagatcggaaatcaatcagctctagaactaacacaggaaca	1701
DB	121	CAGAGAAAACCTGATGTTTWTGGGTATGATGATCATCTTTTGGAGCTTATTAACCTGCACAGC	180
OY	1702	gagcttcgcatctcgctcggtcagtaacagcagaagcagatgttacttactgactggtgca	1761
DB	181	GGGCGCTTGTGATCTTCTGCTTGGCAATGAAAGATGATGATGATGCTTGTGATTGGGTCA	240
OY	1762	aaggaattgtaagaagaagcagtagagatgttagttagatccaatctcaaacaaact	1821
DB	241	AAGGACTTCTGAAGAGAAAAGACTGGATTTCTTGTGATCTGATCTGATCTGCAACCAATTT	300

BASE COUNT	145 a	92 c	129 g	165 t	1 others
ORIGIN	Corvelli."				
Query Match	15.4%: Score 321; DB 79; Length 532;				
Best Local Similarity	75.3%: Pred. No. 2.6e-72;				
Matches	399; Conservative 0; Mismatches 131; Indels 0; Gaps 0;				
QY	1260 catcaaaacctttagattacgaggtctctatagacacccagcagagatgtctgtg 1319				
Db	2 CATCGAATTTCCTTCGCTGCGCTGTGCTGTTTGTATGACACCTACGAAACGGTGTCTTG 61				
QY	1320 tatccttacatgccaatggaagtgttcttcgtgtctcagaagagagccacggtcaaa 1379				
Db	62 TATTCCTTACATGGCTAACGGAAGTGTAGCATCATGTTTACGAAACGCTCAAAATCCAA 121				
QY	1380 ccttcgctgattggccaacgcggaagagaatcgcgcgtacgtacgtcagtcgagttgtct 1439				
Db	122 CCGCCACTTGGCTGGCCAGAACGGAAAGCTATTGCATTGGATCTGCAAGGGGCGTTGCT 181				
QY	1440 taactacatgatcactgcgatcgcgaagatcattcaatccgtygacgtaaagacgacaaac 1499				
Db	182 TATTTTGATGATCATGTTGTGACCCCTTAAGATTATTCACCGATGTCAAAAGCACCTAATATA 241				
QY	1500 cctctagaagcaagaattcogaacggtttgttagagtttcoggttggcgaagtattgac 1559				
Db	242 TTGTTGGACGAAGGAATTTGAAGCAGTGTGTGGAGATTGTTTGCTTAACTTATATGAT 301				
QY	1560 tataaagaacacccagtgcacaacagcagtcggtgcacatcgtgtcacatcgtctccagaa 1619				
Db	302 TATTAAGAATATCTCATGTTACTACTGCTGTAGCTGGAAACAATTGGACATATATACACAGAA 361				
QY	1620 tatctctcaaccggaaaatcttcagaagaaacgcgacgttttcgatacgaatcagttc 1679				
Db	362 TACCTCTCAACTGGAAAGCTTTCACAGAAAGACTGATGTTTGTGATATGCTGTGATGCTT 421				
QY	1680 ctagaactaatcacaggaaacagagcttcgactcgcgtcgcgtcagtcgaagcaagcag 1739				
Db	422 CTTGGAACATAATACCTGGCAAAAGGCGTTTGTATCTACGCTCGACTTGGCCATATATATGAT 481				
QY	1740 gtcattgttactgtgactgggtgaagagattgttgaagagaagaagcctaga 1789				
Db	482 GTCATCTGCTGCTTGATTTGGGCTTAAAGACTTTCANAGACAGCAAAATTGGA 531				
RESULT	6				
LOCUS	AI900110 538 bp mRNA EST 06-DEC-1999				
DEFINITION	scoloid4.y1 Gm-cl012 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl012-871 5' similar to TR-023921 023921 SOMATIC EMBRYOGENESIS				

BASE COUNT	169	a	124	c	179	g	183	t
ORIGIN								
Query Match	13.7%;		Score	286.6;		DB	46;	
Best Local Similarity	66.0%;		Pred.	No. 2.le-63;				
Matches	415;	Conservative	0;	Mismatches	214;	Indels	0;	Gaps
								0
Oy	1056	aagagggttctccttgccggagactcaagatggcgagatgatgggttttagtaacaagaacatt	1115					
Db	4	AAAAGATTTTCACATGGCGGAGAAATTGCACAATTCGTGAACCTGTAAATTTTCAGTGAAGAAAAAGTTT	63					
Oy	1116	ttgggcgaagtggtgttttggaagaagtctaacaaggacacctggcagaagacccttgtt	1175					
Db	64	CTTGCAACAGAGGGGGCTTTGGGAAGAATATAAAGAGSACTTCCAGATAGCAGCTAACAAATT	123					
Oy	1176	gctgtcaagaagactgaagaaagacgaagcgaactccaagttggaagcttcagttcaaacaaa	1235					
Db	124	GCTTAATAACGGTTAACTGATTCAGAAATCTCCGTGGGAGAGGCTGCTTTCCTGCGTAG	183					
Oy	1236	gttagagaatgaatgtatgtgcagacttcaaacacgcttgagaatacagaggttcgtatg	1295					
Db	184	GTTAGCTGATTAAGTGTGTGCAAGTCCACGGAAATCTTTTAAGATTAATTGGTTCTGTACA	243					
Oy	1296	acacgcacccgaagatatgtctgtgtatcccttaacatggccaatgaaagtgtctcgtgt	1355					
Db	244	ACACAACACAGACGCCCTGCTTGTATTCCTTACATGACGAATCTAAGTGTGGCTACACGT	303					
Oy	1356	ctcagaagaaggccacccgttcaacactccgtctgttttttgccaagcggaaagaatcggc	1415					
Db	304	CTACGACAAATTTAAACCTGGGGAGCCAAATATTAGATTGGTCTGC AAGSAGCAGATGGCT	363					
Oy	1416	ctagagctcgaactcgagagttgtlctlaeccatactgaactcgaactcgcgaagaatcatcac	1475					
Db	364	AATGACACAGACTCGTGACTGAGTAFATGACACGACACATCGAATCTTAAGATTATACAT	423					
Oy	1476	cgtagactaaagaagcaagaacaacatccctctagacgaagaattcgaagcggtttgttgagat	1535					
Db	424	CGTACACGTCAAGGCTGCGCAATGCTTTCCTTCATGAAGGTTTTGAACCGGTTGGTGAT	483					
Oy	1536	ttcgggttggcnaagacttatgaactaagaagacatcgaactcgttacacaacagcagtcgtgc	1595					
Db	484	TTCGGCTTGGCAAGCTGGTGGATGTACAGAAAGACATCTGTACATCACAGSTCOGTGA	543					
Oy	1596	accatcggcatacatcgctccagaatatctctcaaccggaaaaactcttcagagaaaaacgac	1655					
Db	544	ACTATGGGTACACATTTGCCCTGAATTTTGTCCACATCGGAAATCATCCGAGAACACGAT	603					
Oy	1656	gtttcggatagcaatcatcagctctcaga	1684					
Db	604	GTTTTGTATACGGCATAAATGCTTTCGA	632					
RESULT	8							
LOCUS	AI896277	555 bp	mRNA	EST	27-JUL-1999			
DEFINITION	EST265720 tomato callus, TBMU Lycopersicon esculentum cDNA clone							
ACCESSION	GI896277							
VERSION	AI896277.1	GI:5602179						
KEYWORDS	EST.							
SOURCE	Lycopersicon esculentum							
ORGANISM	tomato.							
REFERENCE	Lycopersicon esculentum							
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Holt,I.E., Liang,F., Updon,J., Craven,M.B., Bowman,C.L., Ann,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue							
TITLE								

JOURNAL Unpublished (1999)
 COMMENT On May 18, 1998 this sequence version replaced gi:3137451.
 Contact: David Frisch
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 4366
 Fax: 864 656 4299
 Email: dfisch@clemson.edu
 5 prime sequence.

FEATURES
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 Location/Qualifiers
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 /organism="Lycopersicon esculentum"
 /cultivar="TA96"
 /db_xref="taxon:4081"
 /clone="cLECI4J5"
 /clone_lib="tomato callus, TAMU"
 /tissue_type="callus"
 /dev_stage="25-40 days old"
 /lab_host="XL1-Blue MRP"
 /note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Giovannoni laboratory; circ - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus Est Library"

BASE COUNT 154 a 90 c 148 g 163 t
 ORIGIN

Query Match 12.6%; Score 263.4; DB 62; Length 555;
 Best Local Similarity 67.3%; Pred. No. 2e-57;
 Matches 372; Conservative 0; Mismatches 181; Indels 0; Gaps 0.

Oy 1113 atttgagcagagtggtgttggaagagctcaagaagacgttggcagaagcaactc 1172
 Db 1 ATTTGGGTAGCGCGAGATTGGAGTTGTGTCACAGGGCCGCTTAATATGGAAGTGC 60
 Oy 1173 gtgtgttcaagaagacttgaagaagacgaactccaggttgagagcttcagttcaaca 1232
 Db 61 GTGGCTGTCAAAAGATTAAAGCACTACATGCTGTGGTGTGAATTCATTTACAGACA 120
 Oy 1233 gaagtagagtagtaagtttggaagtttcaagaacccgttgagattacagagtttcgt 1292
 Db 121 GAACTTAGTTGATAGTTGGGGGTTCAACGAATCTTCCGTCCTTTGGGTTTTGT 180
 Oy 1293 atgcacacgcagcagagatgtcttgtgtaccccttcaatgagcacaatggaagtgtgtctg 1352
 Db 181 TCACCTGAAGTGAAGGGCTTCTGTTTACCCCTATATGCCAATATGGAAGTGTACGACA 240
 Oy 1353 tgtctcagagagaagcgcaacctcaacctccgcttgaattggccaagcggaagaagata 1412
 Db 241 CGATTAATAAANTATATCCATGCGACGGCCAGTTTGGATGCTGCTCAAGCGGAAAGGATA 300
 Oy 1413 ggcgtagagccagctcgaagttgtcttccctacatagtatcaactcgatccgaagatcatt 1472
 Db 301 GCACTAGGTACACGACAGAGGGGCTAGTATTTTGGATGACGAATGTGACCCCAATATATC 360
 Oy 1473 caaccgtgaagtaagcagaacaacatccctcttagaagagaattcogaagcggtgttgga 1532
 Db 361 CATCGTATGTGAAGAGGACCAATCTCTGTGTGATGTGAGATTTGAAGCGAGTGTGGGA 420
 Oy 1533 gatttcgggttgcaagccttagagcctataaagcactcagcgtgaacaagcagatccgt 1592
 Db 421 GATTTTGGGTTACCAAAAGCTTATAGTACACCGGATTTCTCATGTATACGACATGCGTATAG 480
 Oy 1593 ggcacatcggtaacatcagctccagaatactctcaacoggaaatactcaaganaaac 1652
 Db 481 GGCAACAATTGTGATCAATTTGCTCCAAAATATCTTCTCAACGGGTCAATGCTCGAAGAACT 540
 Oy 1653 gacgcttccgat 1665
 Db 541 GATGTGTTGGATT 553

	Df	169	GGACAGATGTGACAACCTCAAGTTCGCCGGGACATATGGACACTFACCACCCGAGTACTTCT	248
OY	1627	caaccggaataatcttcagagaagaacgcgaactgttccgatacggaaatcatgcttttagaac	1686	
Df	249	CCACTGGGGAAGTCATCAGCAAGAAGAGCATGTCCTTTGGTATTGGATTTATGCTTACAGAC	308	
OY	1687	taatacagagaagaagaagcttccgcttcgcctcgctagctaagcagcagcgcfrcaagt	1746	
Df	309	TTCGTACAGGGTCAACGTGCATTAATGATTTCTCACGCTTGGAAGATGAAGATGATGTTCTTC	368	
OY	1747	tacttgactgggtgaaaaggattgtttgaagagaagaagctagatagttaagtgaagctccag	1806	
Df	369	TTCCTGACTATGTCAANNAACCTGAAAGGGAGAAAACCTGATGCTATCGTAGATCAATA	428	
OY	1807	attctcaacaacaactacgagagagagaagcacygaacaagtatacaagtgcgttgtctat	1866	
Df	429	AACCTTAATATAAAAAATTATCACCATGAGGAGACGTTTAAAGCATGATGCAGATGCTT	488	
OY	1867	gaagccaagagatcaccaatgatgaagaaccaagaatgtctgaagttaaagatgcctggaag	1926	
Df	489	GCACCCCAACCCCTCCCCAAAAGAACCTCCGGGAATTTTCGAAGCTGTTAAGAATCCTGGAG	548	
OY	1927	gagatgyggctgcgcgagaagaatggga	1951	
Df	549	GAAACAGGCGCTCCCCCAAAGGTGGA	573	
RESULT 11				
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DEFINITION	EST244774 tomato ovary, TAMU Lycopersicon esculentum cDNA clone			
ACCESSION	AI486453			
VERSION	AI486453.1	GI:4381824		
KEYWORDS	EST.			
SOURCE	Tomato.			
ORGANISM	Lycopersicon esculentum			
REFERENCE	Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	euphyllipites; Spermatophyta; Magnoliophyta; eudicotyledons; core			
	eudicots; Asteridae; euasterids I; solanales; Solanaceae; Solanum;			
	Lycopersicon.			
TITLE	1 (bases 1 to 471)			
JOURNAL	Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,			
COMMENT	Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., FujiI,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato carpel tissue Unpublished (1999) On May 7, 1998 this sequence version replaced gi:3121325. Contact: David Frisch Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366 Fax: 864 656 4293 Email: df@rsch.clemson.edu.			
FEATURES	Location/Qualifiers			
source	1..471			
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	/db_xref="taxon:4081"			
	/clone="cLEP862"			
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	/tissue_type="carpel"			
	/dev_stage="5 days pre-anthesis to 5 days post-anthesis"			
	/lab_host="XLI-Blue MRP"			
	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLED - Tomato Carpel EST library. OligodT-primed and directionally cloned cDNA in vector Lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."			
BASE COUNT	136 a 88 c 112 g 135 t			

ORIGIN	Query Match	10.7%	Score 222.8	DB 47	Length 471
	Best Local Similarity	67.4%	Pred. No. 5,66-47		
	Matches 314	Conservative	0	Mismatches 152	Indels 0
					Gaps 0
OY	1312	tgcttgatgtctctcttcacatgcgcacatgtaagatggttcgtctgctgcttaagagaagccac	1371		
DB	4	TGCTAGATATCCCATATATGCAAAATTTAAAGTGGTCTATACGCTACAGCACTTAAC	63		
OY	1372	cgtaacaaccctcgcttgattgcccacgcgcgaagaagatcgcgtclagctcagctcgag	1431		
DB	64	CTGGGGAGCCTGTTTTGAATGTGGCCAACTAGGAACCGTGTGGGTGGGTACGCAACG	123		
OY	1432	gtttgtcttaacatcatgatcatcgatcgatcgagaatcattaccgylgacgyltaaacgcg	1491		
DB	124	GACTTGAATACCTACATGCAACACTGTAAACCAAAATTTATTCACCGTGAATTAAGCAG	183		
OY	1492	caaacatccctcttaagccgaagaatctgaagcggtgtgttggaagattcttggtttgcaaac	1551		
DB	184	CTAATGTGTTACTAGATGAGAGATTTTGAAGCTGTGTTGGTGGATTTTGCCCTGGCAAC	243		
OY	1552	ttatgagactaaagaacactcacgylgacacagcagctccgylgacacatcgtgcacatcg	1611		
DB	244	TAGTTGACGTTTAAAGAAACCAATGTACTACTACAGTTCTGTGATACATAGGCCATATAG	303		
OY	1612	ctcgaagatctctcttaacccggaatactctagagaaacccgaagcttttcgatacgaa	1671		
DB	304	CTCTGATATCTTATCCACTGCGGCAATCATGCAAAAACATGATGTTTGGCTATGGA	363		
OY	1672	tcatgctcttagaacactaacacagcaacaagagcttctgactctgcctcgctcagcaag	1731		
DB	364	TCATGCTTTTGAATATGTACCGGCAACGTGCAATAGACTTCTCAGCGCTGAAGANG	423		
OY	1732	acgaagcagctcatgcttacttgactgagtgaggaagatcttgaagaa	1777		
DB	424	AAGATGATGTTCTGTTGCTGCAGACATGTCGAAACCTGCAAGGA	469		
RESULT 12					
LOCUS	A1416897	474 bp	mRNA	EST	01-DEC-1999
DEFINITION	sa196ell.x1 gm-cl005 glycine max cdna clone GENOME SYSTEMS CLONE ID: gm-cl005-165.3' similar to TR-023921 023921 SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE. ; mRNA sequence.				
ACCESSION	A1416897				
VERSION	A1416897.1	GI:4260401			
KEYWORDS	EST.				
SOURCE	soybean.				
ORGANISM	Glycine max				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.				
AUTHORS	1 (bases 1 to 474)				
REFERENCES	Shoenaker, R., Keim, P., Vodkin, L., Epeiding, J., Corryell, V., Kianina, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.				
TITLE	Public Soybean EST Project				
JOURNAL	unpublished (1999)				
COMMENT	On May 7, 1998 this sequence version replaced gi:3119924. Other ESTs: sa196ell.y1				
	Contact: Shoemaker R/Public Soybean EST Project				
	Public Soybean EST Project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: est@wustl.edu				


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RESULT 14
LOCUS A1487272 568 bp mRNA EST 29-JUN-1999
DEFINITION EST245594 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLEDI1M7, mRNA sequence.
ACCESSION A1487272
VERSION A1487272.1 GI:4382643
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 568)
REFERENCE 1
AUTHORS Alcala,J., Vrebalov,J., White,R., Matera,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
JOURNAL Unpublished (1999)
COMMENT On May 18, 1998 this sequence version replaced gi:3136952.
TITLE Contact: David Frisch
JOURNAL Clemson University Genomics Institute
COMMENT Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfisch@CLEMSON.EDU.
FEATURES
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/organism="Lycopersicon esculentum"
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XhoI; cLED - Tomato Carpel EST library. OligodT-primed and
directionally cloned cDNA in vector lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 162 a 125 c 90 g 191 t
ORIGIN
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Best Local Similarity 64.9%; Pred. No. 8.3e-44;
Matches 312; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 267 tctgtaattggaagtgatgcttgcatacttgaaggttactctagttatccaac 326
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DB 88 TCCACAAATCTCAAGGAGCTGCTTGCAATTCCTTGAGAACCAAACTTCTGACCAAAA 147
QY 327 aatgcttgagaagctggaatcctacgctgaagatcctggaatcagatcgtccat 386
|| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 148 AATGCTCTCAAAAGCTGGAGCCCTACACTTGTAATCCTTGACATGAGTTTCATGTACC 207
QY 387 tgaacaacagagacagtgatcataagagttgattggaagatcagatcgtccat 446
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DB 208 TGTGACTCAATATATATATGTTATTCGCTGGATTCGCAATTCATATTTCTGSAACA 267
QY 447 ttatgctcagagctgtgtgtcagaattgcagatttgagattgagcttaacaac 506
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DB 268 TTGAGCAACCAAACTTGCTGTAACCAAGAACTACACTATCTGGAATCTTATAGTATAAC 327
QY 507 ataatgcccagctctagtaatacttgaaactcgaacaactagtgattgattctt 566
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DB 328 TTGAGAGCGCAATCCCAAGGAATTTGGTGAATCTTGAAATCTTATGTAGCATGACCTA 387

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QY 567 tacttaacagctctccggtccattcccggaatcattgggaagaagcttcaagctgaga 626
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DB 388 TATGGCAACAAATTTGAAGGCAACATTCCTCCGACTTTTCCTTAACATAAGTCTTTAA 447
QY 627 ttcttcgagcttaacaacagatcctcactgagtgatctctctatgtcactgaccattt 686
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DB 448 TTTTACGGTTAAACGACAAATGAATGAATGATGTTCTTAACACAATTTGTGGAACAATCCCTGCTGAT 507
QY 687 actaccctcaagtgtagatctatcaataacagactcctgtgttcagttcctgacaat 746
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DB 508 CCAACCTTAAGATTTGATTTGATTTCTTAACACAATTTGTGGAACAATCCCTGCTGAT 567
QY 747 g 747
DB 568 g 568
RESULT 15
LOCUS B09168 1202 bp DNA GSS 14-MAY-1997
DEFINITION T2E10-T7 TAMU Arabidopsis thaliana genomic clone T2E10, genomic
survey sequence.
ACCESSION B09168
VERSION B09168.1 GI:2090299
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
1 (bases 1 to 1202)
REFERENCE 1
AUTHORS Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
Ecker,J.
TITLE BAC End Sequences at ATGC
JOURNAL Unpublished (1997)
COMMENT Other GSSs: T2E10-Sp6
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenomc.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 76
High quality sequence stop: 704.
FEATURES
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ORIGIN
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Best Local Similarity 75.0%; Pred. No. 1.2e-43;
Matches 273; Conservative 0; Mismatches 90; Indels 1; Gaps 1;
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DB 339 TAATTTTCAATCTCTGAGATGACCGACGAGAGGATCTCTGAGTTCACTTGCGGCGCACTTA 398
QY 1057 agaggttcttcttcgagagctacaagtgcgagtgatggtttagtaacaagaacattt 1116

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QY 1117 tgggcaaggltgggttgggaaagtcacaaggagcgttggcagaagcactctgtg 1176
Db 459 TGGGCCGAGGTGGGTTCGGAAGTCTACAAAGGCCCTCTTGCTGATGGAACACTGTGTG 518
QY 1177 ctgtcaagagactgaaggaagagcgaaactccaggltgagagctccagltcaaacagaag 1236
Db 519 CAGTCAAAACGGCTTAAAGAAAGAGCGAACCAGGTGGGAGCTCCAGTTTCAGACAGAAAG 578
QY 1237 taagatgataagatagtcagttcatcgaacctgttgagattacgaggttctgtatg- 1296
Db 579 TGGAGATGATTAGCATGGCCGCTTCACAGATATCTCTCAGGCTTACNTGGGTCTGATAGA 638
QY 1296 acaccgaacgagagatctgtgtatccttacaatggccaatggaagtgtgtcgtgc 1355
Db 639 ACCCTTACCGAAGAAGATGCTTNGTTATCTTAAACATGCTAAGGGAATGTGGCTTCTGT 698
QY 1356 ctca 1359
Db 699 TTGA 702
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Search completed: June 23, 2000, 19:06:57
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